STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 139487

TO: Terra Gibbs **Location: REM-2D10/2C18** **Art Unit: 1635** **Friday, December 03, 2004** **Case Serial Number: 10/024369**	**From: Paul Schulwitz** **Location: Biotech-Chem Library** **REM-1A65** **Phone: (571)272-2527** **paul.schulwitz@uspto.gov**

Search Notes

Examiner Gibbs,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is ____.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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Schreiber, David

From: Gibbs, Terra
Sent: Tuesday, November 16, 2004 10:15 AM
To: Schreiber, David
Subject: Sequence search request...

Hi David,
I have another request for a score over length search:
I need a length limited nucleotide sequence search of nucleobases 1018-1037 of SEQ ID NO:3 in USSN 10/024,369, where the returns are rank ordered based on the score over length/ratio as we've discussed.
I need the lengths limited to hits between 8 and 50 nucleotides, and I'll take as many hits as you can import into excel (64,000?), and alignments for anything above .75 on the above ratio. Hope this is clear, please call me if it's not. I also need the interference databases searched.

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
Mailbox 2C18
571-272-0758

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GenCore version 5.1.6

QM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:38:34 ; Search time 0.001 Seconds
(without alignments)
37.240 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cttctgcccaagaaggtggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 88 seqs, 931 residues

Total number of hits satisfying chosen parameters: 176

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 88 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	12	60.0	15	1	BD061440	ACCESSION:BD061440
c	2	10	50.0	11	1	AX623364	ACCESSION:AX623364
c	3	10	50.0	11	1	AX630785	ACCESSION:AX630785
	4	9.4	47.0	11	1	CQ835700	ACCESSION:CQ835700
	5	9.4	47.0	11	1	AX472203	ACCESSION:AX472203
	6	9	45.0	10	1	BD238992	ACCESSION:BD238992
	7	9	45.0	10	1	BD239512	ACCESSION:BD239512
	8	9	45.0	10	1	BD239813	ACCESSION:BD239813
	9	9	45.0	11	1	CQ836692	ACCESSION:CQ836692
c	10	9	45.0	11	1	AR353840	ACCESSION:AR353840
c	11	9	45.0	11	1	AX625163	ACCESSION:AX625163
c	12	9	45.0	11	1	AX632584	ACCESSION:AX632584
c	13	9	45.0	12	1	AR349259	ACCESSION:AR349259
c	14	9	45.0	12	1	AR349261	ACCESSION:AR349261
	15	8.4	42.0	10	1	A92569	ACCESSION:A92569
	16	8.4	42.0	10	1	AR043677	ACCESSION:AR043677
c	17	8.4	42.0	10	1	BD238844	ACCESSION:BD238844
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	19	8.4	42.0	10	1	BD240663	ACCESSION:BD240663
	20	8.4	42.0	10	1	CQ766709	ACCESSION:CQ766709
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	22	8.4	42.0	10	1	AX152798	ACCESSION:AX152798
	23	8.4	42.0	10	1	AX301616	ACCESSION:AX301616
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	25	8.4	42.0	10	1	AX805907	ACCESSION:AX805907
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	41	8.4	42.0	11	1	CQ836261	ACCESSION:CQ836261
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c	61	8.4	42.0	11	1	AX628191	ACCESSION:AX628191
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	64	8.4	42.0	11	1	AX630798	ACCESSION:AX630798
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ALIGNMENTS

RESULT 1
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LOCUS BD061440 15 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for selectively separating living cell expressed with specific gene.
ACCESSION BD061440
VERSION BD061440.1 GI:22607046
KEYWORDS JP 2001286285-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ishibashi,K. and Tsuji,A.

```
  TITLE     Method for selectively separating living cell expressed with
            specific gene
  JOURNAL   Patent: JP 2001286285-A 2 16-OCT-2001;
            LABORATORY OF MOLECULAR BIOPHOTONICS
COMMENT     OS   Artificial Sequence
            PN   JP 2001286285-A/2
            PD   16-OCT-2001
            PF   28-APR-2000 JP 2000130793
            PI   KANAME ISHIBASHI,AKIHIKO TSUJI
            PC   C12N15/09,C12N1/02,C12N5/10,C12Q1/68,G01N33/48,G01N33/53, PC
            G01N33/566,
            PC   G01N33/58//(C12N1/02,C12R1:91),(C12Q1/68,C12R1:91),C12N15/00,
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Qy       1022 TGCCCAAGAAGG 1033
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Db         14 TGCCCAAGAAGG 3


RESULT 2
AX623364/c
LOCUS       AX623364                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 405 from Patent WO02053774.
ACCESSION   AX623364
VERSION     AX623364.1  GI:28451305
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 405 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES                Location/Qualifiers
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Qy       1024 CCCAAGAAGG 1033
             ||||||||||
Db         10 CCCAAGAAGG 1


RESULT 3
AX630785/c
LOCUS       AX630785                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7826 from Patent WO02053774.
ACCESSION   AX630785
VERSION     AX630785.1  GI:28458825
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7826 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES                Location/Qualifiers
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Qy       1024 CCCAAGAAGG 1033
             ||||||||||
Db         10 CCCAAGAAGG 1


RESULT 4
CQ835700
LOCUS       CQ835700                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 758 from Patent WO2004059001.
ACCESSION   CQ835700
VERSION     CQ835700.1  GI:50835234
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 758 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES                Location/Qualifiers
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Qy       1021 CTGCCCAAGAA 1031
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Db         1 CTGCCCTAGAA 11


RESULT 5
AX472203
LOCUS       AX472203                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 194 from Patent WO02053775.
ACCESSION   AX472203
VERSION     AX472203.1  GI:22207240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hustert,E., Haberl,M. and Wojnowski,L.
  TITLE     Identification of the genetic determinants of the polymorphic
            cyp3a5 expression
  JOURNAL   Patent: WO 02053775-A 194 11-JUL-2002;
            EPIDAUROS BIOTECHNOLOGIE AG (DE)
FEATURES                Location/Qualifiers
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Qy       1020 TCTGCCCAAGA 1030
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Db          1 TCTGCCAAAGA 11


RESULT 6
BD238992
LOCUS       BD238992                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238992
VERSION     BD238992.1  GI:33048762
KEYWORDS    JP 2002534056-A/410.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 410 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/410
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Qy       1029 GAAGGTGGG 1037
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Db          1 GAAGGTGGG 9


RESULT 7
BD239512
LOCUS       BD239512                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239512
VERSION     BD239512.1  GI:33049282
KEYWORDS    JP 2002534056-A/930.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 930 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
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            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
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            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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FEATURES             Location/Qualifiers
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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCA 1027
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Db          2 TTCTGCCCA 10


RESULT 8
BD239813
LOCUS       BD239813                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239813
VERSION     BD239813.1  GI:33049583
KEYWORDS    JP 2002534056-A/1231.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1231 15-OCT-2002;
            GENZYME CORP
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COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1231
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
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            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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Qy       1028 AGAAGGTGG 1036
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Db          2 AGAAGGTGG 10


RESULT 9
CQ836692
LOCUS       CQ836692                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 1750 from Patent WO2004059001.
ACCESSION   CQ836692
VERSION     CQ836692.1  GI:50836226
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 1750 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
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                     /db_xref="taxon:9606"

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  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
              |||||||||
Db          2 AGAAGGTGG 10


RESULT 10
AR353840/c
LOCUS       AR353840                  11 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 15 from patent US 6593111.
ACCESSION   AR353840
VERSION     AR353840.1  GI:33759907
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Baric,R.S. and Yount,B.
  TITLE     Directional assembly of large viral genomes and chromosomes
  JOURNAL   Patent: US 6593111-A 15 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .11
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  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
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Qy       1025 CCAAGAAGG 1033
              |||||||||
Db         10 CCAAGAAGG 2


RESULT 11
AX625163/c
LOCUS       AX625163                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2204 from Patent WO02053774.
ACCESSION   AX625163
VERSION     AX625163.1  GI:28453104
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2204 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

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  Best Local Similarity   100.0%;  Pred. No. 18;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCC 1026
              |||||||||
Db          9 CTTCTGCCC 1


RESULT 12
AX632584/c
LOCUS       AX632584                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9626 from Patent WO02053774.
ACCESSION   AX632584
VERSION     AX632584.1  GI:28468199
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9626 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
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Qy       1018 CTTCTGCCC 1026
              |||||||||
Db          9 CTTCTGCCC 1


RESULT 13
AR349259/c
LOCUS       AR349259                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 6 from patent US 6583986.
ACCESSION   AR349259
VERSION     AR349259.1  GI:33749984
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Storti,W.J., Sibley,K., Ovadia,S., Kimball,S. and Falvo,B.
  TITLE     Method and apparatus for managing thermal energy emissions
  JOURNAL   Patent: US 6583986-A 6 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAA 1031
              |||||||||
Db         10 GCCCAAGAA 2


RESULT 14
AR349261/c
LOCUS       AR349261                  12 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6583986.
ACCESSION   AR349261
VERSION     AR349261.1  GI:33749986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Storti,W.J., Sibley,K., Ovadia,S., Kimball,S. and Falvo,B.
  TITLE     Method and apparatus for managing thermal energy emissions
  JOURNAL   Patent: US 6583986-A 8 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAA 1031
              |||||||||
Db         10 GCCCAAGAA 2


RESULT 15
A92569
LOCUS       A92569                    10 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 10 from Patent WO9812320.
ACCESSION   A92569
VERSION     A92569.1  GI:6741228
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Stoecklin,E. and Groner,B.
  TITLE     NUCLEIC ACID CONSTRUCT CODING FOR A PROTEIN COMPLEX FROM A STAT
            PROTEIN AND A NUCLEAR RECEPTOR AND ITS USE
  JOURNAL   Patent: WO 9812320-A 10 26-MAR-1998;
            STOECKLIN ELISABETH (CH); GRONER BERND (CH)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
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  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              | |||||||||
Db          1 TTCCCAAGAA 10


RESULT 16
AR043677
LOCUS       AR043677                  10 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 47 from patent US 5814517.
ACCESSION   AR043677
VERSION     AR043677.1  GI:5964685
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Seidel,H.Martin. and Lamb,I.Peter.
  TITLE     DNA spacer regulatory elements responsive to cytokines and methods
            for their use
  JOURNAL   Patent: US 5814517-A 47 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              | |||||||||
Db          1 TTCCCAAGAA 10


RESULT 17
BD238844/c
LOCUS       BD238844                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238844
VERSION     BD238844.1  GI:33048614
KEYWORDS    JP 2002534056-A/262.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 262 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/262
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
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            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
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Db         10 TGCCCAAGCA 1


RESULT 18
BD239019/c
LOCUS       BD239019                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239019
VERSION     BD239019.1  GI:33048789
KEYWORDS    JP 2002534056-A/437.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 437 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/437
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
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            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
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              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db         10 AAGCAGGTGG 1


RESULT 19
BD240663
LOCUS       BD240663                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240663
VERSION     BD240663.1  GI:33050433
KEYWORDS    JP 2002534056-A/2081.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 2081 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/2081
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
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            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
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           PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
             C12N1/19,
           PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
             G01N37/00,
           PC   C12N15/00,C12N5/00,C12N15/00
           CC   Preparation and use of superior vaccines
           FH   Key             Location/Qualifiers
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           FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
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Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 20
CQ766709
LOCUS       CQ766709                 10 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 65 from Patent WO2004005541.
ACCESSION   CQ766709
VERSION     CQ766709.1  GI:44908939
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.
  TITLE     Diagnostic tests for the detection of peripheral neuropathy
  JOURNAL   Patent: WO 2004005541-A 65 15-JAN-2004;
            Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /note="3-intron/exon, exon 4, gene RAB7"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 21
AR303500/c
LOCUS       AR303500                 10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 225 from patent US 6544736.
ACCESSION   AR303500
VERSION     AR303500.1  GI:31692276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 225 08-APR-2003;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
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  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
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  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              |||| |||||
Db         10 CTGCTCAAGA 1


RESULT 22
AX152798
LOCUS       AX152798                 10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 713 from Patent WO0138577.
ACCESSION   AX152798
VERSION     AX152798.1  GI:14534449
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 713 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 23
AX301616
LOCUS       AX301616                 10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 330 from Patent WO0185941.
ACCESSION   AX301616
VERSION     AX301616.1  GI:17382699
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 330 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10
```

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RESULT 24
AX374630/c
LOCUS       AX374630                10 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 51 from Patent WO0210454.
ACCESSION   AX374630
VERSION     AX374630.1  GI:19169527
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Choi,J.Y., Koshy,B., Kliem,S. and Stephens,J.C.
  TITLE     Haplotypes of the alas2 gene
  JOURNAL   Patent: WO 0210454-A 51 07-FEB-2002;
            Genaissance Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              |||||||| |
Db         10 GCCCAAGATG 1


RESULT 25
AX805907
LOCUS       AX805907                10 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 53 from Patent WO03060163.
ACCESSION   AX805907
VERSION     AX805907.1  GI:38522818
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   van Eijk,M.J. and van Schaik,C.
  TITLE     Discrimination and detection of target nucleotide sequences using
            mass spectrometry
  JOURNAL   Patent: WO 03060163-A 53 24-JUL-2003;
            Keygene N.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="stuffer sequence"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 26
BD161343/c
LOCUS       BD161343                10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161343
VERSION     BD161343.1  GI:27867101
KEYWORDS    JP 2002186482-A/165.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Nagai,S., Matsushima,K. and Hashimoto,S.
  TITLE     Human activated Th1 and Th2 cell expression genes
  JOURNAL   Patent: JP 2002186482-A 165 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002186482-A/165
            PD   02-JUL-2002
            PF   19-DEC-2000 JP 2000385816
            PI   SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC   Human
            activated Th1 and Th2 cell expression genes FH   Key
            Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
              ||||| ||||
Db         10 TTCTGGCCAA 1


RESULT 27
BD166511
LOCUS       BD166511                10 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Human liver disease-expressing genes.
ACCESSION   BD166511
VERSION     BD166511.1  GI:27872323
KEYWORDS    JP 2002209591-A/56.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
  TITLE     Human liver disease-expressing genes
  JOURNAL   Patent: JP 2002209591-A 56 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002209591-A/56
            PD   30-JUL-2002
            PF   19-JAN-2001 JP 2001012328
            PI   KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO  PI
            YAMASHITA
            PC   C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
            PC   C12P21/08,
            PC   C12N15/00
            CC   Human liver disease-expressing genes
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 28;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10
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RESULT 28
AR074494
LOCUS       AR074494                 11 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 73 from patent US 5955075.
ACCESSION   AR074494
VERSION     AR074494.1  GI:10001249
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 73 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 29
AR081174
LOCUS       AR081174                 11 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 73 from patent US 5972353.
ACCESSION   AR081174
VERSION     AR081174.1  GI:10007902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 73 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 30
AR085371
LOCUS       AR085371                 11 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 73 from patent US 5981711.
ACCESSION   AR085371
VERSION     AR085371.1  GI:10012140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 73 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 31
AR088119
LOCUS       AR088119                 11 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 73 from patent US 5989838.
ACCESSION   AR088119
VERSION     AR088119.1  GI:10014882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 73 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 32
AR104278
LOCUS       AR104278                 11 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 73 from patent US 6093548.
ACCESSION   AR104278
VERSION     AR104278.1  GI:12816986
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 73 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 33
AR143540
LOCUS       AR143540                 11 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 73 from patent US 6204370.
ACCESSION   AR143540
```

```
VERSION     AR143540.1  GI:15104826
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 73 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 34
AR171446
LOCUS       AR171446                  11 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 73 from patent US 6297041.
ACCESSION   AR171446
VERSION     AR171446.1  GI:17910396
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297041-A 73 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 35
AR171617
LOCUS       AR171617                  11 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 73 from patent US 6297051.
ACCESSION   AR171617
VERSION     AR171617.1  GI:17910567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297051-A 73 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 36
BD243207
LOCUS       BD243207                  11 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  MN gene and protein.
ACCESSION   BD243207
VERSION     BD243207.1  GI:33052977
KEYWORDS    JP 2002528085-A/56.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 56 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002528085-A/56
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 2000578465
            PR   23-OCT-1998 US    09/177776,23-OCT-1998 US    09/178115 PI
            JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
            C07K14/47,
            PC   C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
            CC   MN gene and protein
            FH   Key             Location/Qualifiers
            FT   source          1. .11
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 37
CQ833089/c
LOCUS       CQ833089                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 460 from Patent WO2004059002.
ACCESSION   CQ833089
VERSION     CQ833089.1  GI:50832696
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 460 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 38
CQ833231/c
LOCUS       CQ833231                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 602 from Patent WO2004059002.
ACCESSION   CQ833231
VERSION     CQ833231.1  GI:50832838
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining the homeostasis of hairy skin
  JOURNAL   Patent: WO 2004059002-A 602 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              |||||||| |
Db         10 CTGCCCAAAA 1


RESULT 39
CQ835108
LOCUS       CQ835108                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 166 from Patent WO2004059001.
ACCESSION   CQ835108
VERSION     CQ835108.1  GI:50834642
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 166 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 40
CQ835129
LOCUS       CQ835129                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 187 from Patent WO2004059001.
ACCESSION   CQ835129
VERSION     CQ835129.1  GI:50834663
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 187 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 41
CQ836261
LOCUS       CQ836261                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 1319 from Patent WO2004059001.
ACCESSION   CQ836261
VERSION     CQ836261.1  GI:50835795
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 1319 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              ||||| ||||
Db          2 CTGCCAAAGA 11


RESULT 42
CQ837388/c
LOCUS       CQ837388                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 2446 from Patent WO2004059001.
ACCESSION   CQ837388
VERSION     CQ837388.1  GI:50836922
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 2446 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              |||| |||||
Db         11 AGAAAGTGGG 2


RESULT 43
CQ837393
LOCUS       CQ837393                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 2451 from Patent WO2004059001.
ACCESSION   CQ837393
VERSION     CQ837393.1  GI:50836927
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 2451 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              ||||| ||||
Db         2 GCCCAGGAAG 11


RESULT 44
CQ837792/c
LOCUS       CQ837792                  11 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 2850 from Patent WO2004059001.
ACCESSION   CQ837792
VERSION     CQ837792.1  GI:50837326
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
  TITLE     Method for determining markers of human facial skin
  JOURNAL   Patent: WO 2004059001-A 2850 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db         10 AAGCAGGTGG 1


RESULT 45
I34822
LOCUS       I34822                    11 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 15 from patent US 5599673.
ACCESSION   I34822
VERSION     I34822.1  GI:2087790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Keating,M.T., Curran,M.E. and Wang,Q.
  TITLE     Long QT syndrome genes
  JOURNAL   Patent: US 5599673-A 15 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db         1 AGGAGGTGGG 10


RESULT 46
AX412934/c
LOCUS       AX412934                  11 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 698 from Patent WO0222675.
ACCESSION   AX412934
VERSION     AX412934.1  GI:21445392
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 698 21-MAR-2002;
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
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              || |||||||
Db         11 TTTTGCCCAA 2


RESULT 47
AX470593
LOCUS       AX470593                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 170 from Patent WO02053773.
ACCESSION   AX470593
VERSION     AX470593.1  GI:22205718
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 170 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 48
AX471678/c
LOCUS       AX471678                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1255 from Patent WO02053773.
ACCESSION   AX471678
VERSION     AX471678.1  GI:22206803
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1255 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 49
AX471682/c
LOCUS       AX471682                  11 bp    DNA     linear   PAT 09-AUG-2002
DEFINITION  Sequence 1259 from Patent WO02053773.
ACCESSION   AX471682
VERSION     AX471682.1  GI:22206807
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hofmann,K., Conradt,M. and Petersohn,D.
  TITLE     Method for determining skin stress or skin ageing in vitro
  JOURNAL   Patent: WO 02053773-A 1259 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              ||| ||||||
Db         11 CAATAAGGTG 2


RESULT 50
AX623377
LOCUS       AX623377                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 418 from Patent WO02053774.
ACCESSION   AX623377
VERSION     AX623377.1  GI:28451318
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 418 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              |||||| |||
Db          2 CAAGAAAGTG 11


RESULT 51
AX623396/c
LOCUS       AX623396                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 437 from Patent WO02053774.
ACCESSION   AX623396
VERSION     AX623396.1  GI:28451337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 437 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
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                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              |||||| |||
Db         11 AGAAGGCGGG 2


RESULT 52
AX623509
LOCUS       AX623509                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 550 from Patent WO02053774.
ACCESSION   AX623509
VERSION     AX623509.1  GI:28451450
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 550 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db          1 AAGGAGGTGG 10


RESULT 53
AX625581
LOCUS       AX625581                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 2622 from Patent WO02053774.
ACCESSION   AX625581
VERSION     AX625581.1  GI:28453522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 2622 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              || ||||||
Db          1 AAAAAGGTGG 10


RESULT 54
AX626059/c
LOCUS       AX626059                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3100 from Patent WO02053774.
ACCESSION   AX626059
VERSION     AX626059.1  GI:28454097
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3100 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              |||| |||||
Db         11 AGAAAGTGGG 2


RESULT 55
AX626126
LOCUS       AX626126                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3167 from Patent WO02053774.
ACCESSION   AX626126
VERSION     AX626126.1  GI:28454164
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3167 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 56
AX626949/c
LOCUS       AX626949                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3990 from Patent WO02053774.
ACCESSION   AX626949
VERSION     AX626949.1  GI:28454987
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 3990 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
              | ||||||||
Db         10 TCCTGCCCAA 1


RESULT 57
AX627089
LOCUS       AX627089                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4130 from Patent WO02053774.
ACCESSION   AX627089
VERSION     AX627089.1  GI:28455127
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4130 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              ||||||| ||
Db          2 TGCCCAAAAA 11


RESULT 58
AX627751
LOCUS       AX627751                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4792 from Patent WO02053774.
ACCESSION   AX627751
VERSION     AX627751.1  GI:28455789
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4792 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 59
AX627792/c
LOCUS       AX627792                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4833 from Patent WO02053774.
ACCESSION   AX627792
VERSION     AX627792.1  GI:28455830
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4833 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 60
AX627837/c
LOCUS       AX627837                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 4878 from Patent WO02053774.
ACCESSION   AX627837
VERSION     AX627837.1  GI:28455875
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 4878 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db         10 AAGCAGGTGG 1
```

```
RESULT 61
AX628191/c
LOCUS       AX628191                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5232 from Patent WO02053774.
ACCESSION   AX628191
VERSION     AX628191.1  GI:28456229
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5232 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              ||| ||||||
Db         11 CAATAAGGTG 2


RESULT 62
AX628263/c
LOCUS       AX628263                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 5304 from Patent WO02053774.
ACCESSION   AX628263
VERSION     AX628263.1  GI:28456301
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 5304 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
              |||| |||||
Db         11 TTCTACCCAA 2


RESULT 63
AX629947
LOCUS       AX629947                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 6988 from Patent WO02053774.
ACCESSION   AX629947
VERSION     AX629947.1  GI:28457985
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 6988 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 64
AX630798
LOCUS       AX630798                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7839 from Patent WO02053774.
ACCESSION   AX630798
VERSION     AX630798.1  GI:28458838
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7839 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              |||||| |||
Db          2 CAAGAAAGTG 11


RESULT 65
AX630817/c
LOCUS       AX630817                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7858 from Patent WO02053774.
ACCESSION   AX630817
VERSION     AX630817.1  GI:28458857
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7858 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              |||||| |||
Db         11 AGAAGGCGGG 2


RESULT 66
AX630930
LOCUS       AX630930                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 7971 from Patent WO02053774.
ACCESSION   AX630930
VERSION     AX630930.1  GI:28458972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 7971 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db          1 AAGGAGGTGG 10


RESULT 67
AX632853/c
LOCUS       AX632853                  11 bp    DNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 9895 from Patent WO02053774.
ACCESSION   AX632853
VERSION     AX632853.1  GI:28468468
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE     Method for determining homeostasis of the skin
  JOURNAL   Patent: WO 02053774-A 9895 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 26;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAAG 1029
              | ||||||||
Db         11 TGTGCCCAAG 2


RESULT 68
AX480947/c
LOCUS       AX480947                   9 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 7 from Patent WO0246412.
ACCESSION   AX480947
VERSION     AX480947.1  GI:22217586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rebar,E., Jamieson,A., Liu,Q., Liu,P.Q., Wolffe,A., Eisenberg,S.P.
            and Jarvis,E.
  TITLE     Regulation of angiogenesis with zinc finger proteins
  JOURNAL   Patent: WO 0246412-A 7 13-JUN-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="target"

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCA 1027
              ||||||||
Db          8 TCTGCCCA 1


RESULT 69
AX668629
LOCUS       AX668629                   9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2078 from Patent WO0242459.
ACCESSION   AX668629
VERSION     AX668629.1  GI:29291602
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2078 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match            40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity  100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
              ||||||||
Db          1 AAGGTGGG 8


RESULT 70
AX668630
LOCUS       AX668630                   9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2079 from Patent WO0242459.
ACCESSION   AX668630
VERSION     AX668630.1  GI:29291603
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2079 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          1 AAGGTGGG 8


RESULT 71
AX668813
LOCUS       AX668813                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2262 from Patent WO0242459.
ACCESSION   AX668813
VERSION     AX668813.1  GI:29291788
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2262 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          2 AGAAGGTG 9


RESULT 72
AX668814
LOCUS       AX668814                  9 bp    DNA     linear   PAT 26-MAR-2003
DEFINITION  Sequence 2263 from Patent WO0242459.
ACCESSION   AX668814
VERSION     AX668814.1  GI:29291789
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Liu,Q.
  TITLE     Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
  JOURNAL   Patent: WO 0242459-A 2263 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="example target DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          2 AGAAGGTG 9


RESULT 73
AB012724/c
LOCUS       AB012724                  9 bp    DNA     linear   PRI 30-JUN-1998
DEFINITION  Homo sapiens gene for endothelin-A receptor, cis_element region.
ACCESSION   AB012724
VERSION     AB012724.1  GI:3273319
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Hosoda,K., Nakao,K., Tamura,N., Arai,H., Ogawa,Y., Suga,S.,
            Nakanishi,S. and Imura,H.
  TITLE     Organization, structure, chromosomal assignment, and expression of
            the gene encoding the human endothelin-A receptor
  JOURNAL   J. Biol. Chem. 267 (26), 18797-18804 (1992)
  MEDLINE   92406798
   PUBMED   1326535
REFERENCE   2  (sites)
  AUTHORS   Yamashita,J., Yoshimasa,T., Arai,H., Hiraoka,J., Takaya,K.,
            Miyamoto,Y., Ogawa,Y., Itoh,H. and Nakao,K.
  TITLE     Identification of cis-elements of the human endothelin-A receptor
            gene and inhibition of the gene expression by the decoy strategy
  JOURNAL   J. Biol. Chem. 273 (26), 15993-15999 (1998)
  MEDLINE   98298101
   PUBMED   9632648
REFERENCE   3  (bases 1 to 9)
  AUTHORS   Yamashita,J., Yoshimasa,T., Arai,H., Itoh,H. and Nakao,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-1998) Jun Yamashita, Kyoto University Graduate
            School of Medicine, Department of Medicine and Clinical Science; 54
            Shogoin Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan
            (E-mail:juny@kuhp.kyoto-u.ac.jp, Tel:81-75-751-3170,
            Fax:81-75-771-9452)
FEATURES             Location/Qualifiers
     source          1. .9
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     misc_feature    1. .9
                     /note="cis_element of the human endothelin-A receptor
                     gene"

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          9 AAGGTGGG 2


RESULT 74
A15662/c
LOCUS       A15662                   10 bp    DNA     linear   PAT 10-FEB-1994
DEFINITION  oligonucleotide.
ACCESSION   A15662
VERSION     A15662.1  GI:489794
KEYWORDS    .
SOURCE      synthetic construct
```

```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Verrips,C.T., Ledeboer,A.M., Edens,L., Klok,R. and Maat,J.
  TITLE     DNA sequences encoding various allelic forms of mature thaumatin,
            recombinant plasmids comprising said DNA's and a process for their
            preparation, bacterial cultures comprising said recombinant
            plasmids, and method for producing mature thaumatin
  JOURNAL   Patent: EP 0054330-A 4 23-JUN-1982;
            UNILEVER NV; UNILEVER PLC
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db          9 GAAGGTGG 2


RESULT 75
BD238780/c
LOCUS       BD238780                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238780
VERSION     BD238780.1  GI:33048550
KEYWORDS    JP 2002534056-A/198.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 198 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/198
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          8 TTCTGCCC 1


RESULT 76
BD238878/c
LOCUS       BD238878                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238878
VERSION     BD238878.1  GI:33048648
KEYWORDS    JP 2002534056-A/296.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 296 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/296
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
            19-JUN-1998 US    60/090042,19-JUN-1998 US    60/090036 PR
            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
            19-JUN-1998 US    60/090080,19-JUN-1998 US    60/089833 PR
            19-JUN-1998 US    60/089994,19-JUN-1998 US    60/090077 PR
            19-JUN-1998 US    60/090078,19-JUN-1998 US    60/090047 PR
            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
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Db          9 AGAAGGTG 2


RESULT 77
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BD238880/c
LOCUS       BD238880                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD238880
VERSION     BD238880.1  GI:33048650
KEYWORDS    JP 2002534056-A/298.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 298 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/298
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
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Qy       1030 AAGGTGGG 1037
             ||||||||
Db         10 AAGGTGGG 3


RESULT 78
BD239283
LOCUS       BD239283                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239283
VERSION     BD239283.1  GI:33049053
KEYWORDS    JP 2002534056-A/701.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 701 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/701
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC   C12N15/00,C12N5/00,C12N15/00
            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
             ||||||||
Db          2 CTTCTGCC 9


RESULT 79
BD239952/c
LOCUS       BD239952                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239952
VERSION     BD239952.1  GI:33049722
KEYWORDS    JP 2002534056-A/1370.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1370 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1370
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI    BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC    C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC    C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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            PC    C12N15/00,C12N5/00,C12N15/00
            CC    Preparation and use of superior vaccines
            FH    Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
             ||||||||
Db          8 CTTCTGCC 1


RESULT 80
BD240374/c
LOCUS       BD240374                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240374
VERSION     BD240374.1  GI:33050144
KEYWORDS    JP 2002534056-A/1792.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1792 15-OCT-2002;
            GENZYME CORP
COMMENT     OS    Homo sapiens (human)
            PN    JP 2002534056-A/1792
            PD    15-OCT-2002
            PF    18-JUN-1999 JP 2000554749
            PR    19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
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            19-JUN-1998 US    60/089999,19-JUN-1998 US    60/090043 PR
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            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            19-JUN-1998 US    60/090076,19-JUN-1998 US    60/090045 PR
            08-DEC-1998 US    60/111715
            PI    BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC    C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC    C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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            CC    Preparation and use of superior vaccines
            FH    Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
             ||||||||
Db          8 CAAGAAGG 1


RESULT 81
BD240388
LOCUS       BD240388                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240388
VERSION     BD240388.1  GI:33050158
KEYWORDS    JP 2002534056-A/1806.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1806 15-OCT-2002;
            GENZYME CORP
COMMENT     OS    Homo sapiens (human)
            PN    JP 2002534056-A/1806
            PD    15-OCT-2002
            PF    18-JUN-1999 JP 2000554749
            PR    19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
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            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            08-DEC-1998 US    60/111715
            PI    BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC    C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
              C12N1/19,
            PC    C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
              G01N37/00,
            PC    C12N15/00,C12N5/00,C12N15/00
            CC    Preparation and use of superior vaccines
            FH    Key             Location/Qualifiers
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FEATURES              Location/Qualifiers
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                      /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db          2 CTTCTGCC 9


RESULT 82
BD240561
LOCUS       BD240561                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD240561
VERSION     BD240561.1  GI:33050331
KEYWORDS    JP 2002534056-A/1979.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Roberts,B.L. and Shankara,S.
  TITLE     Preparation and use of superior vaccines
  JOURNAL   Patent: JP 2002534056-A 1979 15-OCT-2002;
            GENZYME CORP
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002534056-A/1979
            PD   15-OCT-2002
            PF   18-JUN-1999 JP 2000554749
            PR   19-JUN-1998 US    60/090039,19-JUN-1998 US    60/090040 PR
            19-JUN-1998 US    60/090041,19-JUN-1998 US    60/089853 PR
            19-JUN-1998 US    60/089997,19-JUN-1998 US    60/090079 PR
            19-JUN-1998 US    60/090035,19-JUN-1998 US    60/089993 PR
            19-JUN-1998 US    60/089992,19-JUN-1998 US    60/090072 PR
            19-JUN-1998 US    60/089878,19-JUN-1998 US    60/089991 PR
            19-JUN-1998 US    60/090000,19-JUN-1998 US    60/090048 PR
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            19-JUN-1998 US    60/090044,19-JUN-1998 US    60/089844 PR
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            08-DEC-1998 US    60/111715
            PI   BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC   C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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            PC   C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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            CC   Preparation and use of superior vaccines
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db          2 GAAGGTGG 9


RESULT 83
I19168
LOCUS       I19168                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 31 from patent US 5502176.
ACCESSION   I19168
VERSION     I19168.1  GI:1599523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Tenen,D.G., Pahl,H.L. and Burn,T.C.
  TITLE     Myeloid cell specific promoter
  JOURNAL   Patent: US 5502176-A 31 26-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db          1 CTTCTGCC 8


RESULT 84
I19170
LOCUS       I19170                    10 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 33 from patent US 5502176.
ACCESSION   I19170
VERSION     I19170.1  GI:1599525
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Tenen,D.G., Pahl,H.L. and Burn,T.C.
  TITLE     Myeloid cell specific promoter
  JOURNAL   Patent: US 5502176-A 33 26-MAR-1996;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          3 TTCTGCCC 10


RESULT 85
AR303345
LOCUS       AR303345                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 70 from patent US 6544736.
ACCESSION   AR303345
VERSION     AR303345.1  GI:31692121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and
            Watahiki,M.
  TITLE     Method for synthesizing cDNA from mRNA sample
  JOURNAL   Patent: US 6544736-A 70 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1019 TTCTGCCC 1026
             ||||||||
Db          3 TTCTGCCC 10


RESULT 86
AX152217/c
LOCUS       AX152217                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 132 from Patent WO0138577.
ACCESSION   AX152217
VERSION     AX152217.1  GI:14533868
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 132 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
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Db          8 CAAGAAGG 1


RESULT 87
AX153242
LOCUS       AX153242                  10 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1157 from Patent WO0138577.
ACCESSION   AX153242
VERSION     AX153242.1  GI:14534893
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
  TITLE     Human transcriptomes
  JOURNAL   Patent: WO 0138577-A 1157 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          3 AGAAGGTG 10


RESULT 88
AX301610
LOCUS       AX301610                  10 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 324 from Patent WO0185941.
ACCESSION   AX301610
VERSION     AX301610.1  GI:17382693
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Versteeg,R. and Caron,H.N.
  TITLE     Myc targets
  JOURNAL   Patent: WO 0185941-A 324 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
             ||||||||
Db          2 CTTCTGCC 9


Search completed: December  3, 2004, 11:38:34
Job time : 0.001 secs
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:40:33 ; Search time 0.001 Seconds
(without alignments)
83.680 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cttctgcccaagaaggtggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 195 seqs, 2092 residues

Total number of hits satisfying chosen parameters: 390

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 195 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	20	1	AAL62417	Human ABC transpor
c	2	12	60.0	15	1	ABA96458	Human IL-2 probe S
	3	11.8	59.0	15	1	AAF45929	IGFBP2 oligonucleo
	4	11.4	57.0	15	1	AAF45927	IGFBP2 oligonucleo
	5	11.4	57.0	15	1	AAF45928	IGFBP2 oligonucleo
	6	11	55.0	13	1	ABC34320	Oligonucleotide SE
c	7	11	55.0	13	1	ABC34321	Oligonucleotide SE
	8	11	55.0	13	1	ABC45614	Oligonucleotide SE
c	9	11	55.0	13	1	ABC45615	Oligonucleotide SE
	10	10	50.0	10	1	AAZ81481	Metastatic breast
c	11	10	50.0	11	1	ABV70040	Human skin EST 782
c	12	10	50.0	11	1	ABV62619	Human skin EST 405
c	13	10	50.0	12	1	ABH76170	Oligonucleotide pr
c	14	10	50.0	12	1	ABI71877	Oligonucleotide pr
	15	10	50.0	13	1	AAA54180	5' exon-intron jun
c	16	9.8	49.0	13	1	ABC48640	Oligonucleotide SE
	17	9.8	49.0	13	1	ABC48641	Oligonucleotide SE
	18	9.8	49.0	13	1	ABF26997	Oligonucleotide SE
c	19	9.8	49.0	13	1	ABF26996	Oligonucleotide SE
	20	9.4	47.0	11	1	ABK99486	Human CYP3A5 gene
	21	9.4	47.0	11	1	ADQ32668	Human facial skin-
c	22	9.4	47.0	12	1	ABI13302	Oligonucleotide pr
	23	9.4	47.0	12	1	ABI47015	Oligonucleotide pr
	24	9.4	47.0	12	1	ABI45565	Oligonucleotide pr
	25	9.4	47.0	12	1	ABI69022	Oligonucleotide pr
c	26	9.4	47.0	12	1	ABH91427	Oligonucleotide pr
	27	9.4	47.0	12	1	ABI61189	Oligonucleotide pr
c	28	9.4	47.0	12	1	ABH98731	Oligonucleotide pr
	29	9.4	47.0	12	1	ABH85586	Oligonucleotide pr
	30	9.4	47.0	12	1	ADF78633	Chromosomal abnorm
	31	9	45.0	10	1	AAZ77982	Human dendritic ce
	32	9	45.0	10	1	AAZ78502	Human dendritic ce
	33	9	45.0	10	1	AAZ78803	Human dendritic ce
	34	9	45.0	10	1	AAZ82426	Metastatic breast
	35	9	45.0	10	1	AAF42275	Yeast NORF gene SA
c	36	9	45.0	10	1	ABT14287	Nucleic acid PCR a
c	37	9	45.0	10	1	ADG98610	Human CETP gene al
c	38	9	45.0	11	1	AAA87795	Promoter P15B3 tra
c	39	9	45.0	11	1	AAS07926	Human transcriptio
c	40	9	45.0	11	1	ABV64418	Human skin EST 220
c	41	9	45.0	11	1	ABV71839	Human skin EST 962
c	42	9	45.0	11	1	AAK99270	P15B4 promoter tra
c	43	9	45.0	11	1	AAS21210	Transmissible gast
	44	9	45.0	11	1	ADF30775	Oligonucleotide pr
	45	9	45.0	11	1	ADQ33660	Human facial skin-
	46	9	45.0	12	1	ABI19388	Oligonucleotide pr
	47	9	45.0	12	1	ABI08577	Oligonucleotide pr
	48	9	45.0	12	1	ABI25588	Oligonucleotide pr
	49	9	45.0	12	1	ABI13144	Oligonucleotide pr
c	50	9	45.0	12	1	ABI48769	Oligonucleotide pr
c	51	9	45.0	12	1	ABH88612	Oligonucleotide pr
	52	9	45.0	12	1	ABI67143	Oligonucleotide pr
c	53	9	45.0	12	1	ABH94365	Oligonucleotide pr
c	54	9	45.0	12	1	ABH96358	Oligonucleotide pr
	55	9	45.0	12	1	ABH74429	Oligonucleotide pr
	56	9	45.0	12	1	ABH70993	Oligonucleotide pr
c	57	9	45.0	12	1	ABH88613	Oligonucleotide pr
c	58	9	45.0	12	1	ABI52693	Oligonucleotide pr
	59	9	45.0	12	1	ABI40468	Oligonucleotide pr
	60	9	45.0	12	1	ABI10163	Oligonucleotide pr
c	61	9	45.0	12	1	ABH94363	Oligonucleotide pr
	62	9	45.0	12	1	ABI73341	Oligonucleotide pr
c	63	9	45.0	12	1	AAD25619	MLLCy5L LNA probe
c	64	9	45.0	12	1	AAD25617	MLLCy5P PNA probe
c	65	9	45.0	12	1	ADP28540	Human secreted pro
	66	8.4	42.0	10	1	AAT14161	Cytokine responsiv
	67	8.4	42.0	10	1	AAV56888	Regulatory element
	68	8.4	42.0	10	1	AAZ79653	Human dendritic ce
c	69	8.4	42.0	10	1	AAZ77834	Human dendritic ce
c	70	8.4	42.0	10	1	AAZ78009	Human dendritic ce
	71	8.4	42.0	10	1	AAZ84938	Metastatic breast
c	72	8.4	42.0	10	1	AAZ85708	Metastatic breast
c	73	8.4	42.0	10	1	AAZ81181	Metastatic breast
c	74	8.4	42.0	10	1	AAZ80869	Metastatic breast
c	75	8.4	42.0	10	1	AAZ79893	Human dendritic ce
	76	8.4	42.0	10	1	AAA73656	Probe #25 for sequ
	77	8.4	42.0	10	1	AAH63873	Human ubiquitously
c	78	8.4	42.0	10	1	AAF43792	Yeast NORF gene SA
	79	8.4	42.0	10	1	AAF34723	Yeast NORF gene SA
	80	8.4	42.0	10	1	AAF38664	Yeast NORF gene SA
	81	8.4	42.0	10	1	AAF37520	Yeast NORF gene SA
	82	8.4	42.0	10	1	AAF37547	Yeast NORF gene SA
c	83	8.4	42.0	10	1	AAF40919	Yeast NORF gene SA
	84	8.4	42.0	10	1	AAF38830	Yeast NORF gene SA
	85	8.4	42.0	10	1	AAF41899	Yeast NORF gene SA
	86	8.4	42.0	10	1	AAF40814	Yeast NORF gene SA
	87	8.4	42.0	10	1	ABL88354	Human CHRNE gene p
c	88	8.4	42.0	10	1	ABK37010	Human ALAS2 gene a
	89	8.4	42.0	10	1	ABL39516	Human ETFB primer-
c	90	8.4	42.0	10	1	ABL52253	Human PHKG2 prefer
	91	8.4	42.0	10	1	ABL52252	Human PHKG2 prefer
c	92	8.4	42.0	10	1	ABV78454	Human transcriptio
	93	8.4	42.0	10	1	ABV84246	Human mitochondria
	94	8.4	42.0	10	1	ABK23703	Transcript tag DNA
c	95	8.4	42.0	10	1	ABN84506	Rat smooth muscle
c	96	8.4	42.0	10	1	ACA60848	Rat smooth muscle
c	97	8.4	42.0	10	1	ABQ72900	Human GRM8 gene po
c	98	8.4	42.0	10	1	ABK96537	Human PLAU gene, p
	99	8.4	42.0	10	1	ACF04526	Stuffer sequence u
	100	8.4	42.0	10	1	ADI13685	Cytoplasmic tumour
	101	8.4	42.0	10	1	ADM69071	Human TAT protein-
c	102	8.4	42.0	10	1	ADM33249	Oligo SEQ ID 84, u
	103	8.4	42.0	11	1	AAA16595	Human MN gene 5' d
	104	8.4	42.0	11	1	AAA52514	Human MN gene intr
c	105	8.4	42.0	11	1	ABQ87504	Human skin stress/
c	106	8.4	42.0	11	1	ABQ87500	Human skin stress/

107	8.4	42.0	11	1	ABQ86415	Human skin stress/
108	8.4	42.0	11	1	ABV66344	Human skin EST 413
109	8.4	42.0	11	1	ABV62764	Human skin EST 550
110	8.4	42.0	11	1	ABV70185	Human skin EST 797
c 111	8.4	42.0	11	1	ABV62651	Human skin EST 437
112	8.4	42.0	11	1	ABV67006	Human skin EST 479
c 113	8.4	42.0	11	1	ABV67047	Human skin EST 483
114	8.4	42.0	11	1	ABV64836	Human skin EST 262
c 115	8.4	42.0	11	1	ABV67092	Human skin EST 487
c 116	8.4	42.0	11	1	ABV67518	Human skin EST 530
c 117	8.4	42.0	11	1	ABV72108	Human skin EST 989
118	8.4	42.0	11	1	ABV62632	Human skin EST 418
119	8.4	42.0	11	1	ABV65381	Human skin EST 316
c 120	8.4	42.0	11	1	ABV67446	Human skin EST 523
c 121	8.4	42.0	11	1	ABV66204	Human skin EST 399
c 122	8.4	42.0	11	1	ABV65314	Human skin EST 310
c 123	8.4	42.0	11	1	ABV70072	Human skin EST 785
124	8.4	42.0	11	1	ABV69202	Human skin EST 698
125	8.4	42.0	11	1	ABV70053	Human skin EST 783
c 126	8.4	42.0	11	1	ADG88256	A. thaliana pathog
127	8.4	42.0	11	1	ADK41823	Human MN gene intr
c 128	8.4	42.0	11	1	ADQ35643	Human hair-bearing
c 129	8.4	42.0	11	1	ADQ35785	Human hair-bearing
c 130	8.4	42.0	11	1	ADQ34760	Human facial skin-
131	8.4	42.0	11	1	ADQ32076	Human facial skin-
c 132	8.4	42.0	11	1	ADQ34356	Human facial skin-
133	8.4	42.0	11	1	ADQ34361	Human facial skin-
134	8.4	42.0	11	1	ADQ33229	Human facial skin-
135	8.4	42.0	11	1	ADQ32097	Human facial skin-
136	8	40.0	8	1	AAT09397	5'-primer used for
c 137	8	40.0	8	1	AAT09546	3'-primer used for
138	8	40.0	8	1	AAT09415	5'-primer used for
c 139	8	40.0	8	1	AAT09568	3'-primer used for
140	8	40.0	9	1	ABQ71965	Zinc finger protei
141	8	40.0	9	1	ABQ71964	Zinc finger protei
142	8	40.0	9	1	ABQ71781	Zinc finger protei
143	8	40.0	9	1	ABQ71780	Zinc finger protei
c 144	8	40.0	9	1	ACD06034	Human VEGF-targete
c 145	8	40.0	9	1	ACD19256	Human VEGF-targete
146	8	40.0	9	1	ADA64108	Zinc finger target
147	8	40.0	9	1	ADA64291	Zinc finger target
148	8	40.0	9	1	ADA64292	Zinc finger target
149	8	40.0	9	1	ADA64107	Zinc finger target
150	8	40.0	9	1	ADM22799	Synthetic zinc fin
151	8	40.0	9	1	ADM22984	Synthetic zinc fin
152	8	40.0	9	1	ADM22983	Synthetic zinc fin
153	8	40.0	9	1	ADM22800	Synthetic zinc fin
154	8	40.0	10	1	AAZ79378	Human dendritic ce
c 155	8	40.0	10	1	AAZ77868	Human dendritic ce
156	8	40.0	10	1	AAZ78273	Human dendritic ce
c 157	8	40.0	10	1	AAZ78942	Human dendritic ce
c 158	8	40.0	10	1	AAZ77770	Human dendritic ce
c 159	8	40.0	10	1	AAZ77870	Human dendritic ce
c 160	8	40.0	10	1	AAZ79364	Human dendritic ce
161	8	40.0	10	1	AAZ79551	Human dendritic ce
c 162	8	40.0	10	1	AAZ83134	Metastatic breast
c 163	8	40.0	10	1	AAZ81919	Metastatic breast
164	8	40.0	10	1	AAZ84193	Metastatic breast
165	8	40.0	10	1	AAZ82122	Metastatic breast
c 166	8	40.0	10	1	AAZ83647	Metastatic breast
c 167	8	40.0	10	1	AAZ83418	Metastatic breast
168	8	40.0	10	1	AAZ82784	Metastatic breast
c 169	8	40.0	10	1	AAZ85883	Metastatic breast
170	8	40.0	10	1	AAZ86535	Metastatic breast
171	8	40.0	10	1	AAZ81064	Metastatic breast
172	8	40.0	10	1	AAZ83296	Metastatic breast
173	8	40.0	10	1	AAZ84897	Metastatic breast
c 174	8	40.0	10	1	AAZ81128	Metastatic breast
175	8	40.0	10	1	AAZ83682	Metastatic breast
176	8	40.0	10	1	AAZ83851	Metastatic breast
c 177	8	40.0	10	1	AAZ79914	Human dendritic ce
178	8	40.0	10	1	AAH64317	Human ubiquitously
c 179	8	40.0	10	1	AAH63292	Human colon epithe
180	8	40.0	10	1	AAF69638	Human IL4Ralpha ge
181	8	40.0	10	1	AAF35751	Yeast NORF gene SA
c 182	8	40.0	10	1	AAF39472	Yeast NORF gene SA
c 183	8	40.0	10	1	AAF39102	Yeast NORF gene SA
c 184	8	40.0	10	1	AAF41579	Yeast NORF gene SA
185	8	40.0	10	1	AAF43940	Yeast NORF gene SA
186	8	40.0	10	1	AAF34735	Yeast NORF gene SA
187	8	40.0	10	1	AAF34229	Yeast NORF gene SA
188	8	40.0	10	1	AAF37328	Yeast NORF gene SA
189	8	40.0	10	1	ABK24258	Retinaldehyde-bind
190	8	40.0	10	1	ABK23697	Transcript tag DNA
c 191	8	40.0	10	1	AAS16818	Human apolipoprote
c 192	8	40.0	10	1	ADC09948	Optical nucleic ac
193	8	40.0	10	1	ADI13743	Cytoplasmic tumour
194	8	40.0	10	1	ADK13070	Human glioma endot
195	8	40.0	10	1	ADM57243	A thaliana herbici

ALIGNMENTS

```
RESULT 1
AAL62417/c
ID   AAL62417 standard; DNA; 20 BP.
XX
AC   AAL62417;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human ABC transporter MHC I antisense oligonucleotide, ISIS 206598.
XX
KW   ABC transporter; ABCT; major histocompatibility complex; MHC; cytostatic;
KW   hyperproliferative; autoimmune disorder; antisense gene therapy;
KW   inflammation; tumour formation; immunosuppressive; antimicrobial; human;
KW   phosphorothioate backbone; antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051309-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040101.
XX
PR   17-DEC-2001; 2001US-00024369.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Ward DT,  Freier SM;
XX
DR   WPI; 2003-577305/54.
XX
PT   New antisense compound that hybridizes and inhibits the nucleic acid
PT   encoding ABC transporter major histocompatibility complex 1, for treating
PT   diseases or conditions such as a hyperproliferative or autoimmune
PT   disorder.
XX
```

```
PS   Claim 3; Page 81; 112pp; English.
XX
CC   The invention relates to a compound targetted to a nucleic acid molecule
CC   encoding ABC transporter (ABCT) major histocompatibility complex (MHC) 1
CC   where the compound specifically hybridises with the nucleic acid molecule
CC   and inhibits expression of ATM or specifically hybridises with at least a
CC   portion of an active site on the nucleic acid molecule. The invention is
CC   useful for inhibiting the expression of ATM in cells or tissues. The
CC   invention is useful for treating an animal with hyperproliferative or
CC   autoimmune disorder. The invention is useful for diagnostics,
CC   therapeutics, prophylaxis, as research reagents and kits, for
CC   distinguishing functions of various members of a biological pathway and
CC   in antisense gene therapy. The invention is also useful prophylactically
CC   e.g., to prevent or delay infection, inflammation or tumour formation.
CC   The present sequence is an antisense oligo targetted to human ABC
CC   transporter MHC I DNA. This sequence is used to illustrate the method of
CC   the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0.12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCCAAGAAGGTGGG 1037
              ||||||||||||||||||||
Db         20 CTTCTGCCCAAGAAGGTGGG 1


RESULT 2
ABA96458/c
ID   ABA96458 standard; DNA; 15 BP.
XX
AC   ABA96458;
XX
DT   03-APR-2002  (first entry)
XX
DE   Human IL-2 probe SEQ ID NO 2.
XX
KW   Human; IL-2; IL-4; probe; ss.
XX
OS   Homo sapiens.
XX
PN   JP2001286285-A.
XX
PD   16-OCT-2001.
XX
PF   28-APR-2000; 2000JP-00130793.
XX
PR   04-FEB-2000; 2000JP-00028117.
XX
PA   (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
XX
DR   WPI; 2002-134187/18.
XX
PT   Selective separation of live cells expressing a specific gene.
XX
PS   Example; Page 9; 65pp; Japanese.
XX
CC   The invention relates to selectively separating live cells expressing a
CC   specific gene and involves introducing a labelling agent which can label
CC   a specific mRNA in the cells of a live cell group expressing the mRNA.
CC   The method is used for selectively separating live cells expressing a
CC   specific gene. The present sequence is that of a human IL-2 probe
XX
SQ   Sequence 15 BP; 1 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAAGG 1033
              ||||||||||||
Db         14 TGCCCAAGAAGG 3


RESULT 3
AAF45929
ID   AAF45929 standard; DNA; 15 BP.
XX
AC   AAF45929;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #768.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 4 A; 5 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 15;
  Best Local Similarity   86.7%;  Pred. No. 12;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAGGTGGG 1037
              ||||||||||  || |
Db          1 GCCCAAGAAGCTGCG 15


RESULT 4
```

```
AAF45927
ID   AAF45927 standard; DNA; 15 BP.
XX
AC   AAF45927;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #766.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 5 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 15;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAGGTG 1035
              ||||||||||  ||
Db          3 GCCCAAGAAGCTG 15


RESULT 5
AAF45928
ID   AAF45928 standard; DNA; 15 BP.
XX
AC   AAF45928;
XX
DT   30-MAR-2001  (first entry)
XX
DE   IGFBP2 oligonucleotide #767.
XX
KW   Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW   cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW   skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW   IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW   growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
KW   keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW   hyperneovascular condition; hyperplasia; kidney disease;
KW   neovascular condition of the retina; ss.
XX
OS   Homo sapiens.
XX
PN   WO200078341-A1.
XX
PD   28-DEC-2000.
XX
PF   21-JUN-2000; 2000WO-AU000693.
XX
PR   21-JUN-1999;   99US-0140345P.
XX
PA   (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI   Wraight CJ,  Werther GA,  Edmondson SR;
XX
DR   WPI; 2001-041421/05.
XX
PT   Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT   UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT   inhibits or reduces growth factor mediated cell proliferation and/or
PT   inflammation.
XX
PS   Example 6; Page 39; 201pp; English.
XX
CC   The present invention relates to a method for ameliorating the effects of
CC   skin disorders. The method comprises contacting the skin with an
CC   antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC   receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC   inhibiting or reducing growth factor mediated cell proliferation,
CC   inflammation and/or other disorders. The present sequence is an
CC   oligonucleotide which can be used to design the antisense
CC   oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC   F45161). The method is useful for ameliorating the effects of psoriasis,
CC   ichthyosis, pityriasis, ruba, pilaris, serborrhoea, keloids, keratosis,
CC   neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC   hyperneovascular condition such as a neovascular condition of the retina,
CC   brain or skin, growth factor-mediated malignancies, other sclerotic
CC   disease, kidney disease, hyperproliferation of the inside of blood
CC   vessels or any other hyperplasia
XX
SQ   Sequence 15 BP; 5 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 15;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAGGTG 1035
              ||||||||||  ||
Db          2 GCCCAAGAAGCTG 14


RESULT 6
ABC34320
ID   ABC34320 standard; DNA; 13 BP.
XX
AC   ABC34320;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 34337 for detecting SNP TSC0010965.
```

```
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 34337; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
             ||||||||||| 
Db          3 AAGAAGGTGGG 13


RESULT 7
ABC34321/c
ID   ABC34321 standard; DNA; 13 BP.
XX
AC   ABC34321;
XX
DT   20-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 34338 for detecting SNP TSC0010965.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 34338; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
             ||||||||||| 
Db          11 AAGAAGGTGGG 1


RESULT 8
ABC45614
ID   ABC45614 standard; DNA; 13 BP.
XX
AC   ABC45614;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 45631 for detecting SNP TSC0013272.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 45631; 29pp + Sequence Listing; German.
```

```
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              ||||||||||| 
Db          2 AAGAAGGTGGG 12


RESULT 9
ABC45615/c
ID   ABC45615 standard; DNA; 13 BP.
XX
AC   ABC45615;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 45632 for detecting SNP TSC0013272.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 45632; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 1 A; 7 C; 0 G; 5 T; 0 U; 0 Other;

  Query Match             55.0%;  Score 11;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              ||||||||||| 
Db          2 AAGAAGGTGGG 12


RESULT 10
AAZ81481
ID   AAZ81481 standard; DNA; 10 BP.
XX
AC   AAZ81481;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #715.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 77; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
```

```
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAGGT 1034
             ||||||||||
Db          1 CCAAGAAGGT 10


RESULT 11
ABV70040/c
ID   ABV70040 standard; cDNA; 11 BP.
XX
AC   ABV70040;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7826.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 249; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGAAGG 1033
             ||||||||||
Db         10 CCCAAGAAGG 1


RESULT 12
ABV62619/c
ID   ABV62619 standard; cDNA; 11 BP.
XX
AC   ABV62619;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 405.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 37; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGAAGG 1033
             ||||||||||
Db         10 CCCAAGAAGG 1


RESULT 13
ABH76170/c
ID   ABH76170 standard; DNA; 12 BP.
XX
AC   ABH76170;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 276163 for detecting SNP TSC0004105.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 276163; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1027 AAGAAGGTGG 1036
||||||||||
Db 10 AAGAAGGTGG 1

RESULT 14
ABI71877/c
ID ABI71877 standard; DNA; 12 BP.
XX
AC ABI71877;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 371850 for detecting SNP TSC0059032.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 371850; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 50.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTGGG 1037
||||||||||
Db 11 AGAAGGTGGG 2

RESULT 15
AAA54180
ID AAA54180 standard; cDNA; 13 BP.
XX
AC AAA54180;
XX
DT 08-FEB-2001 (first entry)
XX
DE 5' exon-intron junction of exon 3 of BSMAP.
XX
KW Brain specific membrane anchored protein; BSMAP; dopamine; GABA;
KW receptor; agonist; antagonist; central nervous system; CNS;
KW brain disease; chromosome 19; CLF-I; depression; dyslexia; dystonia;
KW eating disorder; epilepsy; migraine; headache; panic disorder;
KW schizophrenia; obsessive disorder; compulsive disorder;
KW amyotrophic lateral sclerosis; multiple sclerosis; Alzheimer's disease;
KW brain tumour; Huntington's disease; Parkinson's disease; stroke; human;
KW exon; intron; ss.
XX
OS Homo sapiens.
XX
PN WO200055317-A1.
XX
PD 21-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-IB000360.
XX
PR 16-MAR-1999; 99EP-00400636.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Elson G, Bonnefoy J, Gauchat J;
XX
DR WPI; 2000-638200/61.
XX
PT Novel nucleic acid encoding Brain-Specific Membrane Anchored Protein
PT useful for treating central nervous system associated disorders and
PT diseases.

```
XX
PS   Disclosure; Page 13; 45pp; English.
XX
CC   Several receptors (dopamine receptors, the 5-HT family of receptors and
CC   GABA receptors) have been shown to be useful targets by agonist and
CC   antagonist compounds to treat and/or prevent CNS disorders. Brain
CC   receptors in general are attractive candidates for finding new therapies
CC   for brain diseases. Human chromosome 19 is a short chromosome with a
CC   relatively high GC content which has been found to be involved in CNS
CC   functions. The gene for type I cytokine receptor homologue CLF-1 was
CC   recently localised to chromosome 19. Unexpectedly seven other exons
CC   coding in the reverse orientation located adjacent to the CLF-1 exons
CC   have also been found. This new gene was designated brain-specific
CC   membrane anchored protein (BSMAP). Antagonistic compounds directed
CC   against BSMAP are useful for preparing medicaments for treating and/or
CC   preventing central nervous system disorders such as depression, dyslexia,
CC   dystonia, eating disorders, epilepsy, migraine, headache, panic disorder,
CC   schizophrenia, obsessive and compulsive disorders, amyotrophic lateral
CC   sclerosis, multiple sclerosis, Alzheimer's disease, brain tumors,
CC   Huntington's disease, Parkinson's disease and stroke
XX
SQ   Sequence 13 BP; 3 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 10;  DB 1;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
                ||||||||||
Db          1 AGAAGGTGGG 10


RESULT 16
ABC48640/c
ID   ABC48640 standard; DNA; 13 BP.
XX
AC   ABC48640;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 48657 for detecting SNP TSC0013839.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 48657; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 32;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCCAAGA 1030
                ||||| ||||| |
Db         13 CTTCTACCCAAAA 1


RESULT 17
ABC48641
ID   ABC48641 standard; DNA; 13 BP.
XX
AC   ABC48641;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 48658 for detecting SNP TSC0013839.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 48658; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 32;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy       1018 CTTCTGCCCAAGA 1030
              ||||| |||||| |
Db          1 CTTCTACCCAAAA 13


RESULT 18
ABF26997
ID   ABF26997 standard; DNA; 13 BP.
XX
AC   ABF26997;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 126994 for detecting SNP TSC0031788.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 126994; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match            49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 32;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAAGAA 1031
              |||| ||||| ||
Db          1 TTCTCCCCAACAA 13


RESULT 19
ABF26996/c
ID   ABF26996 standard; DNA; 13 BP.
XX
AC   ABF26996;
XX
DT   21-FEB-2002  (first entry)
XX
DE   Oligonucleotide SEQ ID NO 126993 for detecting SNP TSC0031788.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 126993; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match            49.0%;  Score 9.8;  DB 1;  Length 13;
  Best Local Similarity  84.6%;  Pred. No. 32;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAAGAA 1031
              |||| ||||| ||
Db         13 TTCTCCCCAACAA 1


RESULT 20
ABK99486
ID   ABK99486 standard; DNA; 11 BP.
XX
AC   ABK99486;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human CYP3A5 gene polymorphic reference DNA sequence #56.
XX
KW   Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;
KW   AIDS; African American; forensic marker; pharmacological; cytostatic;
KW   antidiabetic; anti-HIV; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200253775-A2.
XX
PD   11-JUL-2002.
XX
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PF 21-DEC-2001; 2001WO-EP015290.
XX
PR 28-DEC-2000; 2000EP-00128627.
PR 28-DEC-2000; 2000US-0258684P.
PR 29-DEC-2000; 2000US-0258952P.
PR 16-JAN-2001; 2001EP-00100172.
PR 18-JAN-2001; 2001US-0262859P.
PR 16-AUG-2001; 2001EP-00118884.
PR 16-AUG-2001; 2001US-0312825P.
XX
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
PI Wojnowski L, Haberl M, Hustert E;
XX
DR WPI; 2002-583628/62.
XX
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,
PT cardiovascular diseases, diabetes and AIDS, and for identifying
PT polymorphisms.
XX
PS Example 2; Page 53; 138pp; English.
XX
CC The present invention relates to a new CYP3A5 polynucleotide encoding a
CC polypeptide, where the polynucleotide is capable of hybridising to a
CC CYP3A5 gene. The invention is useful in an in vitro method for
CC identifying a polymorphism. The invention is also useful for useful for
CC diagnosing a disorder related to the presence of a molecular variant of a
CC CYP3A5 or susceptibility to such a disorder, where the disorder is
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.
CC The invention can further be used for the preparation of a diagnostic
CC composition for diagnosing a disease in a subject having a genome
CC comprising a variant allele of the CYP3A5 gene, where the subject is an
CC African American. The molecules of the invention are as forensic markers
CC and in pharmacological studies. The present nucleic acid sequence
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as
CC described in the invention
XX
SQ Sequence 11 BP; 4 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1020 TCTGCCCAAGA 1030
||||||.||||
Db 1 TCTGCCAAAGA 11

RESULT 21
ADQ32668
ID ADQ32668 standard; DNA; 11 BP.
XX
AC ADQ32668;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 758.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 758; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 3 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 47.0%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1021 CTGCCCAAGAA 1031
||||||.||||
Db 1 CTGCCCTAGAA 11

RESULT 22
ABI13302/c
ID ABI13302 standard; DNA; 12 BP.
XX
AC ABI13302;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 313275 for detecting SNP TSC0025624.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.

```
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 313275; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              | |||||||||
Db         11 ATGAAGGTGGG 1


RESULT 23
ABI47015
ID   ABI47015 standard; DNA; 12 BP.
XX
AC   ABI47015;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 346988 for detecting SNP TSC0044863.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 346988; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              | |||||||||
Db          2 AGGAAGGTGGG 12


RESULT 24
ABI45565
ID   ABI45565 standard; DNA; 12 BP.
XX
AC   ABI45565;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 345538 for detecting SNP TSC0044079.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 345538; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy       1027 AAGAAGGTGGG 1037
              ||| |||||||
Db          2 AAGGAGGTGGG 12


RESULT 25
ABI69022
ID   ABI69022 standard; DNA; 12 BP.
XX
AC   ABI69022;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 368995 for detecting SNP TSC0057391.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 368995; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              ||| |||||||
Db          2 AAGTAGGTGGG 12


RESULT 26
ABH91427/c
ID   ABH91427 standard; DNA; 12 BP.
XX
AC   ABH91427;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 291420 for detecting SNP TSC0014786.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 291420; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              ||||||| ||
Db         11 AAGAAGGTAGG 1


RESULT 27
ABI61189
ID   ABI61189 standard; DNA; 12 BP.
XX
AC   ABI61189;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 361162 for detecting SNP TSC0052480.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
```

```
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 361162; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCCAA 1028
              ||||| |||||
Db          2 CTTCTACCCAA 12


RESULT 28
ABH98731/c
ID   ABH98731 standard; DNA; 12 BP.
XX
AC   ABH98731;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 298724 for detecting SNP TSC0018250.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 298724; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              | ||||||||||
Db         11 AGGAAGGTGGG 1


RESULT 29
ABH85586
ID   ABH85586 standard; DNA; 12 BP.
XX
AC   ABH85586;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 285579 for detecting SNP TSC0012359.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 285579; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
```

```
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGGG 1037
              ||||||| |||
Db          2 AAGAAGGAGGG 12


RESULT 30
ADF78633
ID   ADF78633 standard; DNA; 12 BP.
XX
AC   ADF78633;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Chromosomal abnormality detection-related PCR primer 214.
XX
KW   chromosomal abnormality; maternal locus; genetic disorder; foetus;
KW   mutation; translocation; transversion; monosomy; trisomy; trisomy 21;
KW   chromosome 21; Down's Syndrome; anueoplodies; chromosome deletion;
KW   chromosome addition; chromosome amplification; chromosome translocation;
KW   chromosome rearrangement; single nucleotide polymorphism detection;
KW   SNP detection; pregnant female; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003074723-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006198.
XX
PR   01-MAR-2002; 2002US-0360232P.
PR   11-MAR-2002; 2002US-00093618.
PR   08-MAY-2002; 2002US-0378354P.
XX
PA   (DHAL/) DHALLAN R.
XX
PI   Dhallan R;
XX
DR   WPI; 2003-845073/78.
XX
PT   Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
PT   invasively in a fetus, comprises forming a ratio of amounts of alleles at
PT   a locus of interest and a different heterozygous locus.
XX
PS   Example 11; Page 234; 164pp; English.
XX
CC   This invention relates to a novel method of detecting chromosomal
CC   abnormalities by determining the sequence of alleles of a locus of
CC   interest from template DNA, determining which alleles are present and
CC   comparing to amounts of alleles at a different, selected heterozygous
CC   locus (for example on another chromosome or a maternal locus); relative
CC   amounts are expressed as a ratio indicating presence or absence of the
CC   abnormality. The method is useful for the detection of genetic disorders,
CC   especially in a foetus, including chromosomal abnormalities and
CC   mutations, for example translocations, transversions, monosomies,
CC   trisomies (for example trisomy 21 in which an additional copy of
CC   chromosome 21 results in Down's Syndrome) and other anueoplodies,
CC   deletions, additions, amplifications, translocations and rearrangements.
CC   It can be used to detect any alterations in a gene sequence, especially
CC   single nucleotide polymorphisms (SNPs), and may be used to detect
CC   numerous abnormalities simultaneously, for example if several SNPs are
CC   associated with a particular disease. The method provides a rapid, non-
CC   invasive method for determining the sequence of DNA from a foetus using a
CC   sample from a pregnant female, for example to detect genetic disorders as
CC   above or to determine if a foetus is a carrier of a disease or
CC   predisposed to a disease.
XX
SQ   Sequence 12 BP; 3 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 37;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCCAA 1028
              || ||||||||
Db          2 CTACTGCCCAA 12


RESULT 31
AAZ77982
ID   AAZ77982 standard; DNA; 10 BP.
XX
AC   AAZ77982;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:410.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
```

XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 76; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 GAAGGTGGG 1037
|||||||||
Db 1 GAAGGTGGG 9

RESULT 32
AAZ78502
ID AAZ78502 standard; DNA; 10 BP.
XX
AC AAZ78502;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:930.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 92; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,

```
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCA 1027
              |||||||||
Db          2 TTCTGCCCA 10


RESULT 33
AAZ78803
ID   AAZ78803 standard; DNA; 10 BP.
XX
AC   AAZ78803;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1231.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 100; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
              |||||||||
Db          2 AGAAGGTGG 10


RESULT 34
AAZ82426
ID   AAZ82426 standard; DNA; 10 BP.
XX
AC   AAZ82426;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1660.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
```

PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 103; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1018 CTTCTGCCC 1026
|||||||||
Db 2 CTTCTGCCC 10

RESULT 35
AAF42275
ID AAF42275 standard; DNA; 10 BP.
XX
AC AAF42275;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9014.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 321; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1026 CAAGAAGGT 1034
|||||||||
Db 2 CAAGAAGGT 10

RESULT 36
ABT14287/c
ID ABT14287 standard; DNA; 10 BP.
XX
AC ABT14287;
XX
DT 20-FEB-2003 (first entry)
XX
DE Nucleic acid PCR amplification method-related RAPD PCR primer #57.
XX
KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX
OS Unidentified.
XX
PN WO200281743-A2.
XX

PD 17-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-GB001489.
XX
PR 02-APR-2001; 2001GB-00008182.
XX
PA (HAMI/) HAMILL B.
XX
PI Hamill B;
XX
DR WPI; 2003-075484/07.
XX
PT Amplification of nucleotide sequences from polynucleotides by chain
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
PT solution, 2 attached to supports and both share complementary sequences.
XX
PS Disclosure; Fig 17; 60pp; English.
XX
CC The invention comprises a method for the PCR amplification of nucleic
CC acids. The method involves a set of primers, where two of the primers are
CC in solution and at least two other primers are attached to a solid
CC support. The method of the invention can be used for the analysis of a
CC nucleic acid or a mixture of nucleic acids, including: single-stranded
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
CC PCR primer of the invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1022 TGCCCAAGA 1030
||||||||| |
Db 10 TGCCCAAGA 2

RESULT 37
ADG98610/c
ID ADG98610 standard; DNA; 10 BP.
XX
AC ADG98610;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human CETP gene allele specific extension PCR primer #71.
XX
KW human; cholesteryl ester transfer protein; CETP;
KW single nucleotide polymorphism; SNP; drug screening; atherosclerosis;
KW cardiovascular disease; hypercholesterolaemia;
KW allele specific oligonucleotide; ss; extension PCR; primer.
XX
OS Homo sapiens.
XX
PN WO2003091277-A2.
XX
PD 06-NOV-2003.
XX
PF 28-APR-2003; 2003WO-US013288.
XX
PR 26-APR-2002; 2002US-0375791P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Chew A, Kazemi A, Lachowicz M, Lee HH, Parks KE;
PI Petersen N, Rounds E, Sausker EA, Tirrell C;
XX
DR WPI; 2003-865576/80.
XX
PT New isolated polynucleotide useful for haplotyping and/or genotyping
PT cholesteryl ester transfer protein (CETP) gene in an individual or in
PT screening for drugs useful in treating diseases associated with CETP
PT activity.
XX
PS Claim 45; SEQ ID NO 242; 250pp; English.
XX
CC The invention comprises the amino acid and coding sequences of the human
CC cholesteryl ester transfer protein (CETP), the invention also comprises
CC polymorphisms identified within the CETP gene. The DNA and protein
CC sequences of the invention are useful in haplotyping and/or genotyping
CC the CETP gene in an individual. The DNA and protein sequences may also be
CC used to screen drugs or compounds targeting the CETP or its variant to
CC treat a condition or disease associated with CETP (e.g. atherosclerosis,
CC cardiovascular disease or hypercholesterolaemia). The present DNA
CC sequence represents an allele specific extension PCR primer for the human
CC CETP gene.
XX
SQ Sequence 10 BP; 1 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTGG 1036
||||||||| |
Db 9 AGAAGGTGG 1

RESULT 38
AAA87795/c
ID AAA87795 standard; DNA; 11 BP.
XX
AC AAA87795;
XX
DT 28-NOV-2000 (first entry)
XX
DE Promoter P15B3 transcription factor binding site SEQ ID #159.
XX
KW Human; secreted protein; forensic procedure; gene therapy;
KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW mitochondriocytopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW septic shock; impotence; promoter; P15B3; ds.
XX
OS Homo sapiens.
XX
PN WO200037491-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-IB002058.
XX
PR 22-DEC-1998; 98US-0113686P.
PR 25-JUN-1999; 99US-0141032P.
XX
PA (GEST) GENSET.
XX
PI Bougueleret L, Dumas J, Duclert A;
XX
DR WPI; 2000-442637/38.
XX
PT Polynucleotides and polypeptides encoding proteins with signal peptides,
PT useful in diagnostic, forensic, gene therapy and chromosome mapping
PT procedures.
XX
PS Example 48; Fig 5; 306pp; English.
XX
CC This sequence represents a transcription factor binding site identified
CC in the human P15B3 promoter. The invention relates to sequences AAA87725-
CC A87774 which encode human secreted proteins AAB25763-B25812. The proteins
CC include signal peptides. The P15B3 promoter is used in the isolation of
CC the cDNAs of the invention. Included in the invention are a host cell
CC containing one of the cDNA sequences, and a purified antibody capable of

CC binding to one of the secreted proteins. Also contained in the invention
CC are methods for storing the sequence data on a computer system, and a
CC method for identifying features of the cDNA sequences using a computer
CC programme. The cDNAs are useful for expressing secreted proteins or
CC fragments to obtain antibodies capable of specifically binding to the
CC secreted proteins. The cDNAs may also be useful in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondriocytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence
XX
SQ Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 GAAGGTGGG 1037
|||||||||
Db 10 GAAGGTGGG 2

RESULT 39
AAS07926/c
ID AAS07926 standard; DNA; 11 BP.
XX
AC AAS07926;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human transcription factor binding site from promoter P15B4 #5.
XX
KW Human; expressed sequence tag; EST; ds; promoter P15B4;
KW acute myocardial infarction; acute ischaemic stroke; diabetes; anaemia;
KW growth hormone deficiency; hepatitis; kidney carcinoma;
KW multiple sclerosis; chemotherapy-induced neutropaenia;
KW transcription factor binding site.
XX
OS Homo sapiens.
XX
PN EP1104808-A1.
XX
PD 06-JUN-2001.
XX
PF 27-JUL-2000; 2000EP-00202699.
XX
PR 05-AUG-1999; 99US-0147499P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Jobert S, Giordano J;
XX
DR WPI; 2001-357986/38.
XX
PT New purified 5' expressed sequence tags useful in diagnostic, forensic,
PT gene therapy or chromosome mapping procedures, or for distinguishing
PT human tissues or cells from non-human tissues or cells.
XX
PS Example 53; Fig 5; 90pp; English.
XX
CC The sequence represents a transcription factor binding site from human
CC promoter P15B4, the promoter and binding site being isolated using
CC sequence from one of the 5' expressed sequence tags (EST) of the
CC invention, one of 15442 nucleotide sequences not given in the
CC specification. The 5' EST may be used to efficiently identify and isolate
CC 5'untranslated regions (UTRs) and upstream regulatory regions which
CC control the location, developmental stage, rate and quantity of protein
CC synthesis, as well as the stability of the mRNA. ESTs containing the 5'
CC ends of protein genes may include sequences for chromosome mapping and
CC identification individuals. The EST may further be used to distinguish
CC human tissues or cells from non-human tissues or cells, to distinguish
CC between human tissues or cells that do not and do not express
CC polynucleotides comprising the 5' EST sequences, to obtain and express
CC cDNA clones which include full protein coding sequences of the
CC corresponding gene products, to map and clone promoter regions, and open
CC reading frames from a genomic sequence, and to obtain and express
CC extended cDNAs encoding portions of the protein. EST-related nucleic
CC acids are useful in forensic procedures or in diagnosis of genetic
CC diseases resulting from abnormal gene expression, for constructing a high
CC resolution map of human chromosomes, and in gene therapy to control or
CC treat genetic diseases. Proteins expressed from the cDNAs may be used in
CC treating or controlling a variety of human conditions e.g acute
CC myocardial infarction, acute ischaemic stroke, diabetes, anaemia, growth
CC hormone deficiency, hepatitis, kidney carcinoma, multiple sclerosis,
CC chemotherapy-induced neutropaenia
XX
SQ Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 GAAGGTGGG 1037
|||||||||
Db 10 GAAGGTGGG 2

RESULT 40
ABV64418/c
ID ABV64418 standard; cDNA; 11 BP.
XX
AC ABV64418;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 2204.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 86; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

```
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCC 1026
             |||||||||
Db          9 CTTCTGCCC 1


RESULT 41
ABV71839/c
ID   ABV71839 standard; cDNA; 11 BP.
XX
AC   ABV71839;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9625.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 311; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCC 1026
             |||||||||
Db          9 CTTCTGCCC 1


RESULT 42
AAK99270/c
ID   AAK99270 standard; DNA; 11 BP.
XX
AC   AAK99270;
XX
DT   31-MAY-2002  (first entry)
XX
DE   P15B4 promoter transcription binding site DELTAEF1_01.
XX
KW   Promoter DNA; diagnostic; forensic; gene therapy; chromosome mapping;
KW   expression vector; secretion vector; P15B4; transcription binding site;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   CA2343602-A1.
XX
PD   18-OCT-2001.
XX
PF   17-APR-2001; 2001CA-02343602.
XX
PR   18-APR-2000; 2000US-0197873P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards JB,  Jobert S,  Giordano J,  Tanaka H,  Bejanin S;
XX
DR   WPI; 2002-227459/29.
XX
PT   New nucleic acid sequences comprising human expressed sequence tags
PT   (ESTs), useful in diagnostic, forensic, gene therapy or chromosome
PT   mapping procedures, or for designing expression vectors and secretion
PT   vectors.
XX
PS   Disclosure; Fig 5; 163pp; English.
XX
CC   The invention relates to purified nucleic acids, which comprise sequences
CC   selected from any of more than 50000 sequences not defined in the
CC   specification. The polynucleotide sequences are useful in making cDNA,
CC   polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy
CC   or chromosome mapping procedures. The nucleic acid sequences are also
CC   useful for designing expression vectors and secretion vectors. This
CC   polynucleotide sequence represents a P15B4 promoter transcription binding
CC   site of the invention
XX
SQ   Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
             |||||||||
Db         10 GAAGGTGGG 2


RESULT 43
AAS21210/c
ID   AAS21210 standard; DNA; 11 BP.
XX
AC   AAS21210;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transmissible gastroenteritis virus full length clone, C/DE-1 junction.
XX
KW   Transmissible gastroenteritis virus; TGE; gene transfer;
KW   recombinant viral genome; gene therapy; artificial chromosome; vaccine;
KW   ds.
XX
```

```
OS   Transmissible gastroenteritis virus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(6,T)
FT                   /*tag=  a
FT   misc_feature    7. .8
FT                   /*tag=  b
FT                   /label= Cleavage_site
FT                   /note= "Restriction enzyme Bgl1 cleaves at this site
FT                   creating a sticky end"
FT   mutation        replace(10,A)
FT                   /*tag=  c
XX
PN   WO200190340-A2.
XX
PD   29-NOV-2001.
XX
PF   21-MAY-2001; 2001WO-US016564.
XX
PR   21-MAY-2000; 2000US-0206537P.
PR   20-APR-2001; 2001US-0285320P.
XX
PA   (UYNC-) UNIV NORTH CAROLINA.
XX
PI   Baric RS,  Yount B;
XX
DR   WPI; 2002-114288/15.
XX
PT   Directionally assembling a recombinant viral genome, useful for
PT   manipulating the genomes of plants, animals, bacteria or viruses for gene
PT   therapy, by ligating the subclones of the viral genome to assemble a
PT   recombinant viral genome.
XX
PS   Example 7; Page 22; 42pp; English.
XX
CC   The invention describes a method of directionally assembling a
CC   recombinant viral genome comprising ligating the subclones of the viral
CC   genome to assemble a recombinant viral genome, particularly coronavirus.
CC   For directionally assembling a recombinant viral genome. In particular,
CC   the method is useful for manipulating the genomes of higher plants and
CC   animals, as well as bacteria and viruses. In particular, the method is
CC   useful for the precise genetic manipulation of individual chromosomes in
CC   whole plants and animals and the construction of artificial chromosomes
CC   for gene therapy. The genomes produced are useful in preparing vaccines
CC   and expression vectors (e.g., TGE vectors and vaccines), which are useful
CC   in protocols involving vaccination, gene transfer and gene therapy. This
CC   sequence represents the interconnecting junction site C/DE-1 used in the
CC   assembly of the full length transmissible gastroenteritis virus (TGE)
CC   genome described in the method of the invention
XX
SQ   Sequence 11 BP; 0 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAGG 1033
              |||||||||
Db         10 CCAAGAAGG 2


RESULT 44
ADF30775
ID   ADF30775 standard; DNA; 11 BP.
XX
AC   ADF30775;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO:10.
XX
KW   nucleic acid identification; wave pattern generation; dissociation curve;
KW   dissociation curve wave pattern database; single nucleotide polymorphism;
KW   SNP; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003097828-A1.
XX
PD   27-NOV-2003.
XX
PF   20-MAY-2003; 2003WO-JP006275.
XX
PR   21-MAY-2002; 2002JP-00182177.
XX
PA   (ADGE-) ADGENE CO LTD.
XX
PI   Oshima J,  Nemoto K;
XX
DR   WPI; 2004-012534/01.
XX
PT   Method for identifying nucleic acids by constructing dissociation curves
PT   with synthetic nucleic acids.
XX
PS   Example 4; SEQ ID NO 10; 94pp; Japanese.
XX
CC   The present invention describes a method for identifying nucleic acids
CC   by: (1) synthesising nucleic acids that are complementary to different
CC   parts of the target nucleic acid; (2) constructing dissociation curves
CC   for a mixture of the synthetic nucleic acids; and (3) by comparing the
CC   wave patterns, identifying the nucleic acid with the same wave pattern to
CC   have the same base sequence. Also described: (A) primers for wave pattern
CC   generation; (B) producing the primers; (C) a nucleic acid identification
CC   kit; (D) generating wave patterns for the dissociation curves; and (E)
CC   dissociation curve wave pattern database. The method can be used for
CC   nucleic acid identification which is useful in the analysis of single
CC   nucleotide polymorphisms (SNPs). The present sequence represents an
CC   oligonucleotide primer which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 11 BP; 2 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              |||||||||
Db          2 GAAGGTGGG 10


RESULT 45
ADQ33660
ID   ADQ33660 standard; DNA; 11 BP.
XX
AC   ADQ33660;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 1750.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
```

XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 1750; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 4 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTGG 1036
|||||||||
Db 2 AGAAGGTGG 10

RESULT 46
ABI19388
ID ABI19388 standard; DNA; 12 BP.
XX
AC ABI19388;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 319361 for detecting SNP TSC0029179.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 319361; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1027 AAGAAGGTG 1035
|||||||||
Db 1 AAGAAGGTG 9

RESULT 47
ABI08577
ID ABI08577 standard; DNA; 12 BP.
XX
AC ABI08577;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 308550 for detecting SNP TSC0023078.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 308550; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,

```
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTG 1035
              |||||||||
Db          2 AAGAAGGTG 10


RESULT 48
ABI25588
ID   ABI25588 standard; DNA; 12 BP.
XX
AC   ABI25588;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 325561 for detecting SNP TSC0032603.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 325561; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTG 1035
              |||||||||
Db          3 AAGAAGGTG 11


RESULT 49
ABI13144
ID   ABI13144 standard; DNA; 12 BP.
XX
AC   ABI13144;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 313117 for detecting SNP TSC0025502.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 313117; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              |||||||||
Db          4 GAAGGTGGG 12


RESULT 50
ABI48769/c
ID   ABI48769 standard; DNA; 12 BP.
XX
AC   ABI48769;
XX
DT   22-FEB-2002  (first entry)
```

```
XX
DE   Oligonucleotide primer SEQ ID NO 348742 for detecting SNP TSC0045724.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 348742; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              |||||||||
Db         12 GAAGGTGGG 4


RESULT 51
ABH88612/c
ID   ABH88612 standard; DNA; 12 BP.
XX
AC   ABH88612;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 288605 for detecting SNP TSC0013593.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 288605; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTG 1035
              |||||||||
Db          9 AAGAAGGTG 1


RESULT 52
ABI67143
ID   ABI67143 standard; DNA; 12 BP.
XX
AC   ABI67143;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 367116 for detecting SNP TSC0056171.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
```

```
XX
PS   Claim 1; SEQ ID NO 367116; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTG 1035
             |||||||||
Db          1 AAGAAGGTG 9


RESULT 53
ABH94365/c
ID   ABH94365 standard; DNA; 12 BP.
XX
AC   ABH94365;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 294358 for detecting SNP TSC0016077.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 294358; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
             |||||||||
Db          12 AGAAGGTGG 4


RESULT 54
ABH96358/c
ID   ABH96358 standard; DNA; 12 BP.
XX
AC   ABH96358;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 296351 for detecting SNP TSC0017041.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 296351; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
             |||||||||
Db          12 GAAGGTGGG 4
```

```
RESULT 55
ABH74429
ID   ABH74429 standard; DNA; 12 BP.
XX
AC   ABH74429;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 274414 for detecting SNP TSC0003539.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 274414; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              |||||||||
Db          3 GAAGGTGGG 11


RESULT 56
ABH70993
ID   ABH70993 standard; DNA; 12 BP.
XX
AC   ABH70993;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 270970 for detecting SNP TSC0002341.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 270970; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              |||||||||
Db          3 GAAGGTGGG 11


RESULT 57
ABH88613/c
ID   ABH88613 standard; DNA; 12 BP.
XX
AC   ABH88613;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 288606 for detecting SNP TSC0013593.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
```

```
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 288606; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 1 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTG 1035
             |||||||||
Db          9 AAGAAGGTG 1


RESULT 58
ABI52693/c
ID   ABI52693 standard; DNA; 12 BP.
XX
AC   ABI52693;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 352666 for detecting SNP TSC0048025.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 352666; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 4 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
             |||||||||
Db         10 AGAAGGTGG 2


RESULT 59
ABI40468
ID   ABI40468 standard; DNA; 12 BP.
XX
AC   ABI40468;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 340441 for detecting SNP TSC0041530.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 340441; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
```

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  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
              |||||||||
Db          1 AGAAGGTGG 9


RESULT 60
ABI10163
ID   ABI10163 standard; DNA; 12 BP.
XX
AC   ABI10163;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 310136 for detecting SNP TSC0023830.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 310136; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
              |||||||||
Db          4 AGAAGGTGG 12


RESULT 61
ABH94363/c
ID   ABH94363 standard; DNA; 12 BP.
XX
AC   ABH94363;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 294356 for detecting SNP TSC0016077.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 294356; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
              |||||||||
Db         12 AGAAGGTGG 4


RESULT 62
ABI73341
ID   ABI73341 standard; DNA; 12 BP.
XX
AC   ABI73341;
XX
DT   22-FEB-2002  (first entry)
XX
DE   Oligonucleotide primer SEQ ID NO 373314 for detecting SNP TSC0059971.
XX
KW   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW   peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW   central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS   Homo sapiens.
XX
PN   WO200177384-A2.
```

```
XX
PD   18-OCT-2001.
XX
PF   06-APR-2001; 2001WO-IB000713.
XX
PR   07-APR-2000; 2000DE-01019173.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2001-657177/75.
XX
PT   Set of oligonucleotides, useful for diagnosis and cell typing, is
PT   designed to detect single-nucleotide polymorphisms and cytosine
PT   methylation status.
XX
PS   Claim 1; SEQ ID NO 373314; 29pp + Sequence Listing; German.
XX
CC   This invention describes novel oligonucleotide primers or peptide nucleic
CC   acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC   and cytosine methylation status in chemically pretreated genomic DNA. The
CC   oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC   range of diseases including immune system, gastrointestinal, respiratory,
CC   central nervous system, cardiovascular and metabolic disorders. The
CC   oligomers are also used for detecting cell type differentiation. ABC00010
CC   -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC   represent the oligomers described in the invention. NOTE: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
             |||||||||
Db          1 AGAAGGTGG 9


RESULT 63
AAD25619/c
ID   AAD25619 standard; DNA; 12 BP.
XX
AC   AAD25619;
XX
DT   26-MAR-2002  (first entry)
XX
DE   MLLCy5L LNA probe used for haplotyping MLL-AF4/98(+) chimeric gene.
XX
KW   Haplotyping; single molecule detection; luminescent marker;
KW   genetic marker; MLL-AF4/98(+); locked nucleic acid; LNA; probe; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N,N'-biscarboxypentyl-5, 5'-
FT                   disulfonatoindodicarbocyanine (Cy5) fluorophore labelled
FT                   thymine"
XX
PN   WO200190418-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US016394.
XX
PR   22-MAY-2000; 2000US-0206512P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cai H,  Goodwin PM,  Keller RA,  Werner JH;
XX
DR   WPI; 2002-083123/11.
XX
PT   Rapid haplotyping of DNA or RNA segments, comprises labeling at least 2
PT   target sites on a segment of DNA or RNA with separate distinguishable
PT   luminescent hybridization probes.
XX
PS   Example 1; Page 22; 49pp; English.
XX
CC   The invention relates to rapid haplotyping a DNA or RNA segment by single
CC   molecule detection. The method involves labelling at least 2 target sites
CC   on a DNA or RNA segment with separate distinguishable luminescent marker
CC   hybridisation probes, where the targets are selected genetic markers and
CC   detecting the presence or absence of each luminescent hybridisation probe
CC   on each DNA segment to determine the haplotype of each DNA or RNA
CC   segment. The method is useful for rapid haplotyping of DNA or RNA
CC   segment. The present sequence is a locked nucleic acid (LNA) probe used
CC   for haplotyping MLL-AF4/98(+) chimeric gene
XX
SQ   Sequence 12 BP; 0 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAA 1031
             |||||||||
Db         10 GCCCAAGAA 2


RESULT 64
AAD25617/c
ID   AAD25617 standard; DNA; 12 BP.
XX
AC   AAD25617;
XX
DT   26-MAR-2002  (first entry)
XX
DE   MLLCy5P PNA probe used for haplotyping MLL-AF4/98(+) chimeric gene.
XX
KW   Haplotyping; single molecule detection; luminescent marker;
KW   genetic marker; MLL-AF4/98(+); peptide nucleic acid; PNA; probe; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "N,N'-biscarboxypentyl-5, 5'-
FT                   disulfonatoindodicarbocyanine (Cy5) fluorophore labelled
FT                   thymine; This base is linked to the label via linker"
FT   misc_feature    12
FT                   /*tag=  b
FT                   /note= "This base is attached to a linker sequence"
XX
PN   WO200190418-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US016394.
XX
PR   22-MAY-2000; 2000US-0206512P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cai H,  Goodwin PM,  Keller RA,  Werner JH;
XX
DR   WPI; 2002-083123/11.
```

```
XX
PT   Rapid haplotyping of DNA or RNA segments, comprises labeling at least 2
PT   target sites on a segment of DNA or RNA with separate distinguishable
PT   luminescent hybridization probes.
XX
PS   Example 1; Page 22; 49pp; English.
XX
CC   The invention relates to rapid haplotyping a DNA or RNA segment by single
CC   molecule detection. The method involves labelling at least 2 target sites
CC   on a DNA or RNA segment with separate distinguishable luminescent marker
CC   hybridisation probes, where the targets are selected genetic markers and
CC   detecting the presence or absence of each luminescent hybridisation probe
CC   on each DNA segment to determine the haplotype of each DNA or RNA
CC   segment. The method is useful for rapid haplotyping of DNA or RNA
CC   segment. The present sequence is a peptide nucleic acid (PNA) probe used
CC   for haplotyping MLL-AF4/98(+) chimeric gene
XX
SQ   Sequence 12 BP; 0 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAA 1031
              |||||||||
Db         10 GCCCAAGAA 2


RESULT 65
ADP28540/c
ID   ADP28540 standard; DNA; 12 BP.
XX
AC   ADP28540;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Human secreted protein encoding sequence SEQ ID #538.
XX
KW   Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW   cancer; inflammatory; immune; ds; human secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO2004035732-A2.
XX
PD   29-APR-2004.
XX
PF   28-AUG-2003; 2003WO-US026780.
XX
PR   29-AUG-2002; 2002US-0406576P.
PR   29-AUG-2002; 2002US-0406579P.
PR   29-AUG-2002; 2002US-0406585P.
PR   29-AUG-2002; 2002US-0406588P.
PR   29-AUG-2002; 2002US-0406608P.
PR   29-AUG-2002; 2002US-0406611P.
PR   29-AUG-2002; 2002US-0406612P.
PR   29-AUG-2002; 2002US-0406616P.
PR   29-AUG-2002; 2002US-0406640P.
PR   29-AUG-2002; 2002US-0406642P.
PR   29-AUG-2002; 2002US-0406646P.
PR   29-AUG-2002; 2002US-0406653P.
PR   29-AUG-2002; 2002US-0406655P.
PR   29-AUG-2002; 2002US-0406666P.
PR   17-SEP-2002; 2002US-0410946P.
PR   17-SEP-2002; 2002US-0410947P.
PR   17-SEP-2002; 2002US-0410948P.
PR   17-SEP-2002; 2002US-0410949P.
PR   17-SEP-2002; 2002US-0410953P.
PR   17-SEP-2002; 2002US-0410957P.
PR   17-SEP-2002; 2002US-0410958P.
PR   17-SEP-2002; 2002US-0410959P.
PR   17-SEP-2002; 2002US-0410960P.
PR   17-SEP-2002; 2002US-0410961P.
PR   17-SEP-2002; 2002US-0410962P.
PR   17-SEP-2002; 2002US-0411019P.
PR   17-SEP-2002; 2002US-0411022P.
PR   17-SEP-2002; 2002US-0411023P.
PR   17-SEP-2002; 2002US-0411024P.
PR   17-SEP-2002; 2002US-0411032P.
PR   17-SEP-2002; 2002US-0411035P.
PR   17-SEP-2002; 2002US-0411037P.
PR   17-SEP-2002; 2002US-0411041P.
PR   17-SEP-2002; 2002US-0411045P.
PR   17-SEP-2002; 2002US-0411046P.
PR   17-SEP-2002; 2002US-0411048P.
PR   17-SEP-2002; 2002US-0411052P.
PR   17-SEP-2002; 2002US-0411055P.
PR   17-SEP-2002; 2002US-0411073P.
PR   17-SEP-2002; 2002US-0411082P.
PR   17-SEP-2002; 2002US-0411101P.
PR   17-SEP-2002; 2002US-0411111P.
PR   18-APR-2003; 2003US-0463700P.
PR   18-APR-2003; 2003US-0463708P.
PR   18-APR-2003; 2003US-0463716P.
PR   18-APR-2003; 2003US-0463732P.
PR   02-MAY-2003; 2003US-0467199P.
PR   02-MAY-2003; 2003US-0467201P.
PR   02-MAY-2003; 2003US-0467203P.
PR   02-MAY-2003; 2003US-0467230P.
PR   19-MAY-2003; 2003US-0471306P.
PR   19-MAY-2003; 2003US-0471336P.
PR   22-MAY-2003; 2003US-0472420P.
PR   22-MAY-2003; 2003US-0472430P.
PR   09-JUN-2003; 2003US-0476609P.
PR   09-JUN-2003; 2003US-0476641P.
PR   08-JUL-2003; 2003US-0485218P.
PR   08-JUL-2003; 2003US-0485223P.
PR   08-JUL-2003; 2003US-0485224P.
PR   08-JUL-2003; 2003US-0485325P.
PR   14-JUL-2003; 2003US-0486446P.
PR   14-JUL-2003; 2003US-0486480P.
PR   15-JUL-2003; 2003US-0486891P.
PR   15-JUL-2003; 2003US-0486960P.
PR   08-AUG-2003; 2003US-0493341P.
PR   08-AUG-2003; 2003US-0493370P.
PR   08-AUG-2003; 2003US-0493573P.
PR   08-AUG-2003; 2003US-0493577P.
XX
PA   (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
PI   Williams LT,  Chu K,  Lee E,  Hestir K,  Beaurang PA,  Behrens D;
PI   Halenbeck RF,  Huang MM,  Kothakota S,  Haishan L,  Linnemann T;
PI   Pierce K,  Wang Y,  Wong JGP,  Wu G,  Zhang H;
XX
DR   WPI; 2004-348438/32.
XX
PT   New nucleic acid molecule for diagnosing, preventing or treating diseases
PT   such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT   genetic, bacterial and viral diseases.
XX
PS   Claim 1; SEQ ID NO 538; 428pp; English.
XX
CC   The present invention relates to an isolated nucleic acid molecule
CC   encoding a polypeptide which is believed to be cytostatic,
CC   antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC   composition and methods are useful for diagnosing, preventing and
CC   treating diseases such as proliferative (e.g. cancer), inflammatory,
CC   immune, metabolic, genetic, bacterial and viral diseases. The present
CC   sequence represents a human secreted protein encoding sequence. The
CC   present sequence is available on WIPOWEB and is not in the specification.
XX
SQ   Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       1025 CCAAGAAGG 1033
              |||||||||
Db         12 CCAAGAAGG 4
```

RESULT 66
AAT14161
ID AAT14161 standard; DNA; 10 BP.
XX
AC AAT14161;
XX
DT 29-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KW Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KW gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN WO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US004477.
XX
PR 14-APR-1994; 94US-00228935.
PR 27-MAR-1995; 95US-00410780.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Seidel HM, Lamb IP;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for detecting
PT the presence of transcriptional regulatory protein in a sample.
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element TT(Nx)AA,
CC where x is 4-7, and the regulatory element binds an activated
CC transcriptional regulatory protein in response to a signalling mol., i.e.
CC a cytokine. This cytokine responsive DNA spacer regulatory element can be
CC used to detect the presence of a transcriptional regulatory protein in a
CC sample, and in assays for (ant)agonists of gene transcription. The
CC identified cpds. may be used to treat cytokine-induced disease states, or
CC to ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions
XX
SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              | ||||||||
Db          1 TTCCCAAGAA 10
```

RESULT 67
AAV56888
ID AAV56888 standard; DNA; 10 BP.
XX
AC AAV56888;
XX
DT 02-DEC-1998 (first entry)
XX
DE Regulatory element containing oligonucleotide #47.
XX
KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW transcriptional control; STAT protein; screening; agonist; ss.
XX
OS Synthetic.
XX
PN US5814517-A.
XX
PD 29-SEP-1998.
XX
PF 27-MAR-1995; 95US-00410779.
XX
PR 14-APR-1994; 94US-00228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1998-541763/46.
XX
PT DNA constructs containing cytokine-responsive regulatory elements -
PT useful in assays for transcription-regulating proteins or gene
PT transcription agonists or antagonists.
XX
PS Disclosure; Col 12; 58pp; English.
XX
CC AAV56842-V56976 and AAV61601-V61631 are oligonucleotides used in the
CC production of constructs comprising a cytokine-responsive regulatory
CC element linked to a promoter which is linked to a heterologous coding
CC sequence so that the coding sequence is under the transcriptional control
CC of the regulatory element and the promoter, where the regulatory element
CC has a nucleotide sequence selected from TTCNNGAA, TTANyTAA, and TTCNyTAA
CC where N is A, T, C or G, and y = 3 or 4. The constructs can be used to
CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,
CC in a sample by contacting the sample with the construct so that the
CC protein binds to the regulatory element, and detecting or separating the
CC resulting complex. The cells can be used in screening assays for agonists
CC of gene transcription, in which the level of expression of the coding
CC sequence is measured in the presence and absence of a test compound or in
CC the presence of the corresponding cytokine
XX
SQ Sequence 10 BP; 4 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              | ||||||||
Db          1 TTCCCAAGAA 10
```

RESULT 68
AAZ79653
ID AAZ79653 standard; DNA; 10 BP.
XX
AC AAZ79653;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:2081.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.

```
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 124; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 69
AAZ77834/c
ID   AAZ77834 standard; DNA; 10 BP.
XX
AC   AAZ77834;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:262.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
```

```
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 71; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              ||||||||  |
Db         10 TGCCCAAGCA 1


RESULT 70
AAZ78009/c
ID   AAZ78009 standard; DNA; 10 BP.
XX
AC   AAZ78009;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:437.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 77; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
```

```
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db         10 AAGCAGGTGG 1


RESULT 71
AAZ84938
ID   AAZ84938 standard; DNA; 10 BP.
XX
AC   AAZ84938;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4172.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 170; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 72
AAZ85708/c
ID   AAZ85708 standard; DNA; 10 BP.
XX
AC   AAZ85708;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #4942.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 190; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
```

```
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              ||||||| ||
Db         10 GCCCAAGCAG 1


RESULT 73
AAZ81181/c
ID   AAZ81181 standard; DNA; 10 BP.
XX
AC   AAZ81181;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #415.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 69; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              |||||||| |
Db         10 CTGCCCAAAA 1


RESULT 74
AAZ80869/c
ID   AAZ80869 standard; DNA; 10 BP.
XX
AC   AAZ80869;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #103.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 61; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
```

```
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              |||||| |||
Db         10 AGAAGGGGGG 1


RESULT 75
AAZ79893/c
ID   AAZ79893 standard; DNA; 10 BP.
XX
AC   AAZ79893;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell preferentially expressed SAGE tag, SEQ ID NO:184.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-US013820.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 62; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity  90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              |||||||| |
Db         10 TGCCCAAGCA 1


RESULT 76
AAA73656
ID   AAA73656 standard; DNA; 10 BP.
XX
AC   AAA73656;
XX
DT   30-JAN-2001  (first entry)
XX
DE   Probe #25 for sequencing by hybridisation.
XX
KW   Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200040758-A2.
XX
PD   13-JUL-2000.
XX
PF   06-JAN-2000; 2000WO-US000458.
XX
PR   06-JAN-1999;   99US-0115284P.
XX
PA   (HYSE-) HYSEQ INC.
```

```
XX
PI   Drmanac R,  Drmanac S,  Kita D,  Cooke C,  Xu C;
XX
DR   WPI; 2000-475839/41.
XX
PT   Identifying one or more sequences of a target nucleic acid (NA), useful
PT   for parallel analyses, comprises contacting the NA with a set of pools of
PT   probes comprising mixture of probes with different information regions.
XX
PS   Disclosure; Page 53; 196pp; English.
XX
CC   The present sequence is a probe used to demonstrate the method of the
CC   invention, which is concerned with the use of pools of probes to enable
CC   sequencing by hybridisation, a process known as SBH. Overlapping probes
CC   are used which allows the identification of sequences longer then the
CC   probe length, and either the target nucleic acid or the probe is
CC   labelled. The method of the invention is useful for assembling sequences
CC   and in parallel analyses
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAAG 1029
              ||| ||||||
Db          1 TCTCCCCAAG 10


RESULT 77
AAH63873
ID   AAH63873 standard; cDNA; 10 BP.
XX
AC   AAH63873;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 713.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 55; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 78
AAF43792/c
ID   AAF43792 standard; DNA; 10 BP.
XX
AC   AAF43792;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11931.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 376; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
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CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
              |||| |||||
Db         10 TTCTACCCAA 1


RESULT 79
AAF34723
ID   AAF34723 standard; DNA; 10 BP.
XX
AC   AAF34723;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1462.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 52; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAGGT 1034
              | ||||||||
Db          1 CTAAGAAGGT 10


RESULT 80
AAF38664
ID   AAF38664 standard; DNA; 10 BP.
XX
AC   AAF38664;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5403.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 193; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
```

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CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              || |||||||
Db          1 AACAAGGTGG 10


RESULT 81
AAF37520
ID   AAF37520 standard; DNA; 10 BP.
XX
AC   AAF37520;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4259.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 152; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              ||||| ||||
Db          1 CTGCCGAAGA 10


RESULT 82
AAF37547
ID   AAF37547 standard; DNA; 10 BP.
XX
AC   AAF37547;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4286.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 153; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
```

CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1018 CTTCTGCCCA 1027
|||| |||||
Db 1 CTTCAGCCCA 10

RESULT 83
AAF40919/c
ID AAF40919 standard; DNA; 10 BP.
XX
AC AAF40919;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7658.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 273; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1028 AGAAGGTGGG 1037
| ||||||||
Db 10 ATAAGGTGGG 1

RESULT 84
AAF38830
ID AAF38830 standard; DNA; 10 BP.
XX
AC AAF38830;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5569.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 198; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at

```
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          1 AAGAATGTGG 10


RESULT 85
AAF41899
ID   AAF41899 standard; DNA; 10 BP.
XX
AC   AAF41899;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8638.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 308; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              | ||||||||
Db          1 GACCAAGAAG 10


RESULT 86
AAF40814
ID   AAF40814 standard; DNA; 10 BP.
XX
AC   AAF40814;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7553.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 269; 419pp; English.
XX
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CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAGGT 1034
              ||||||| |
Db          1 CCAAGAAGTT 10


RESULT 87
ABL88354
ID   ABL88354 standard; DNA; 10 BP.
XX
AC   ABL88354;
XX
DT   20-MAY-2002  (first entry)
XX
DE   Human CHRNE gene polymorphism detection primer, SEQ ID NO:88.
XX
KW   Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE;
KW   chromosome 17p13-12; acetylcholine receptor; AChR;
KW   neuromuscular junction; skeletal muscle; postnatal development;
KW   congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;
KW   genetic variant; single nucleotide polymorphism; SNP; gene therapy;
KW   drug screening; primer extension; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200198316-A2.
XX
PD   27-DEC-2001.
XX
PF   20-JUN-2001; 2001WO-US019835.
XX
PR   20-JUN-2000; 2000US-0212870P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Amaro E,  Bieglecki KM,  Kliem SE,  Koshy B,  Tanguay DA;
XX
DR   WPI; 2002-130787/17.
XX
PT   Novel genetic variants of cholinergic receptor, nicotinic, epsilon
PT   polypeptide gene useful in studying expression and function of the
PT   protein, and for screening drugs to treat diseases e.g. congential
PT   myasthenic syndrome.
XX
PS   Claim 19; Page 15; 104pp; English.
XX
CC   The invention relates to a method for haplotyping the cholinergic
CC   receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an
CC   individual, and also describes 17 novel polymorphic sites within the
CC   human CHRNE gene. The CHRNE gene is located on chromosome 17p13-12 and
CC   contains 12 exons which encode a 493 amino acid protein (ABB49112). The
CC   CHRNE protein is one of the 5 subunits of mammalian acetylcholine
CC   receptors (AChRs) found at neuromuscular junctions in juveniles and
CC   adults, and is essential for the normal postnatal development of skeletal
CC   muscle. Mutations in the CHRNE gene are associated with congenital
CC   myasthenic syndrome (CMS). CHRNE gene sequences can therefore be used in
CC   gene therapy. The CHRNE gene is also useful for studying the expression
CC   and function of CHRNE, and in expressing CHRNE protein for use in
CC   screening for candidate drugs to treat diseases related to CHRNE. The
CC   method of the invention is useful for haplotyping the CHRNE gene in an
CC   individual, and can also be used in pharmaceutical research to validate
CC   CHRNE as a candidate target for, and in design of clinical trials of
CC   candidate drugs for, treating a specific condition drugs or disease
CC   predicted to be associated with CHRNE activity such as CMS. Polymorphisms
CC   in the target region may be determined by the use of allele-specific
CC   oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by
CC   primer extension using oligonucleotide primers comprising sequences
CC   ABL88371-ABL88354. The CHRNE protein is useful for improving the
CC   efficiency and reliability of several steps in the discovery and
CC   development of drugs for treating diseases associated with CHRNE
CC   activity, and may be used to screen drugs which target CHRNE. Sequences
CC   ABL88321-ABL88354 represent sequences that are specifically claimed as
CC   components of primers used to detect polymorphisms in the CHRNE gene by
CC   primer extension
XX
SQ   Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              |||| |||||
Db          1 AGAACGTGGG 10


RESULT 88
ABK37010/c
ID   ABK37010 standard; DNA; 10 BP.
XX
AC   ABK37010;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human ALAS2 gene allele-specific oligonucleotide PCR primer #9.
XX
KW   Human; aminolevulinate delta synthase 2; ALAS2; haplotyping; primer; ss;
KW   haplotype pair; single nucleotide polymorphism; genotyping; antianaemic;
KW   gene therapy; drug screening; X-linked sideroblastic anaemia; sequencing;
KW   hypochromic anaemia; probe; PCR.
XX
OS   Homo sapiens.
XX
PN   WO200210454-A2.
XX
PD   07-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US023914.
XX
PR   28-JUL-2000; 2000US-0221827P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
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PI Choi JY, Koshy B, Kliem S, Stephens JC;
XX
DR WPI; 2002-188755/24.
XX
PT New isolated human aminolevulinate delta synthase 2 polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the aminolevulinate protein.
XX
PS Claim 18; Page 14; 90pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the gene
CC encoding human aminolevulinate delta synthase 2 (ALAS2). A method for
CC haplotyping the ALAS2 gene in an individual comprises identifying the
CC nucleotide at one or more polymorphic sites and determining whether one
CC of the copies of the gene is defined by one of the ALAS2 haplotypes given
CC in the specification or whether both copies are defined by a haplotype
CC pair. This method is useful in genotyping, whereby all possible haplotype
CC pairs can be assigned to specific genotypes. An association between a
CC trait and a haplotype or haplotype pair of the ALAS2 gene can be
CC identified by comparing the frequency of the haplotype or haplotype pair
CC in a population exhibiting the trait with the frequency of the haplotype
CC or haplotype pair in a reference population, where a higher haplotype
CC frequency in the trait population indicates the trait is associated with
CC the haplotype or haplotype pair. ALAS2 and its corresponding DNA are used
CC for studying the expression and function of ALAS2, for use in screening
CC for candidate drugs to treat diseases related to ALAS2 activity, such as
CC X-linked sideroblastic anaemia and hypochromic anaemia. The sequences are
CC also useful for studying the effect of variation on the biological
CC activity of ALAS2 as well as on the binding affinity of candidate drugs
CC targeting ALAS2. Sequences ABK36963-ABK37027 represent allele-specific
CC oligonucleotide probes, sequencing primers and PCR primers used to detect
CC ALAS2 gene polymorphisms
XX
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1023 GCCCAAGAAG 1032
|||||||| |
Db 10 GCCCAAGATG 1

RESULT 89
ABL39516
ID ABL39516 standard; DNA; 10 BP.
XX
AC ABL39516;
XX
DT 22-APR-2002 (first entry)
XX
DE Human ETFB primer-extension oligonucleotide 22.
XX
KW Human; electron-transfer flavoprotein beta polypeptide; ETFB;
KW electron acceptor; mitochondrial matrix; glutaric acidaemia type II;
KW novel polymorphic site; novel polymorphism; ETFB genotype; ss; GAII;
KW ETFB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.
XX
OS Homo sapiens.
XX
PN WO200202580-A2.
XX
PD 10-JAN-2002.
XX
PF 05-JUL-2001; 2001WO-US021306.
XX
PR 05-JUL-2000; 2000US-0215984P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
XX
DR WPI; 2002-154722/20.
XX
PT Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the flavoprotein.
XX
PS Claim 19; Page 15; 143pp; English.
XX
CC The invention comprises DNA, cDNA and protein sequences of the human
CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC chromosome 19q13.3-13.4). The invention specifically relates to the
CC identification of 27 novel polymorphic sites within the ETFB gene.
CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor
CC for nine primary flavoprotein dehydrogenases and is located in the
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC Deficiency of ETF or ETFDH leads to glutaric acidaemia type II (GAII).
CC Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC GAII. The novel ETFB polymorphisms identified in the invention are useful
CC for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC protein and nucleic acids of the invention are useful for studying the
CC expression and function of ETFB in vivo. The ETFB protein and nucleic
CC acids are also useful for testing the efficacy of therapeutic agents and
CC compounds for glutaric acidaemia type II. The nucleic acids of the
CC invention are useful in the production of a transgenic animal expressing
CC the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC represent claimed ETFB primer-extension oligonucleotides
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1021 CTGCCCAAGA 1030
|| |||||||
Db 1 CTCCCCAAGA 10

RESULT 90
ABL52253/c
ID ABL52253 standard; DNA; 10 BP.
XX
AC ABL52253;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human PHKG2 preferred oligonucleotide primer SEQ ID NO:40.
XX
KW Human; phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;
KW phosphorylase kinase gamma 2; single nucleotide polymorphism;
KW polymorphic; hepatotropic; gene therapy; glycogen storage disease;
KW liver cirrhosis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200194365-A2.
XX
PD 13-DEC-2001.
XX
PF 11-JUN-2001; 2001WO-US018814.
XX
PR 09-JUN-2000; 2000US-0210568P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Choi JY, Koshy B, Sanchis A, Sausker EA;
XX
DR WPI; 2002-404359/43.

```
XX
PT   New variants of phosphorylase kinase gamma 2 isogenes, useful for
PT   improving efficiency and reliability in the development of drugs for
PT   treating diseases e.g. liver cirrhosis.
XX
PS   Claim 18; Page 14; 76pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) comprising
CC   a nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or
CC   its fragment, or a polymorphic variant of a reference sequence for a
CC   PHKG2 cDNA or its fragment. Also described is an isolated polypeptide
CC   (II) comprising an amino acid sequence which is a polymorphic variant of
CC   a reference sequence for PHKG2 protein or its fragment, where the
CC   reference sequence comprises a sequence (see ABB09290) of 406 amino
CC   acids, and the polymorphic variant comprises one or more variant amino
CC   acids selected from glutamic acid at a position corresponding to amino
CC   acid position 153 and tryptophan at position corresponding to amino acid
CC   position 329. (I) has hepatotropic activity and can be used in gene
CC   therapy. (II) is useful in screening for drugs targeting (II), by
CC   contacting a PHKG2 polymorphic variant with a candidate agent and
CC   assaying for binding activity. The identified candidate agents targeting
CC   PHKG2, are useful for treating liver cirrhosis and glycogen storage
CC   diseases. The present sequence represents a preferred oligonucleotide
CC   primer for the PHKG2 gene, which is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 10 BP; 1 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db         10 AGGAGGTGGG 1


RESULT 91
ABL52252
ID   ABL52252 standard; DNA; 10 BP.
XX
AC   ABL52252;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human PHKG2 preferred oligonucleotide primer SEQ ID NO:39.
XX
KW   Human; phosphorylase kinase gamma 2 (testis); PHKG2; enzyme; SNP;
KW   phosphorylase kinase gamma 2; single nucleotide polymorphism;
KW   polymorphic; hepatotropic; gene therapy; glycogen storage disease;
KW   liver cirrhosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200194365-A2.
XX
PD   13-DEC-2001.
XX
PF   11-JUN-2001; 2001WO-US018814.
XX
PR   09-JUN-2000; 2000US-0210568P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Koshy B,  Sanchis A,  Sausker EA;
XX
DR   WPI; 2002-404359/43.
XX
PT   New variants of phosphorylase kinase gamma 2 isogenes, useful for
PT   improving efficiency and reliability in the development of drugs for
PT   treating diseases e.g. liver cirrhosis.
XX
PS   Claim 18; Page 14; 76pp; English.
XX
CC   The present invention describes an isolated polynucleotide (I) comprising
CC   a nucleotide sequence which is a polymorphic variant of a reference
CC   sequence for human phosphorylase kinase gamma2 (testis) (PHKG2) gene or
CC   its fragment, or a polymorphic variant of a reference sequence for a
CC   PHKG2 cDNA or its fragment. Also described is an isolated polypeptide
CC   (II) comprising an amino acid sequence which is a polymorphic variant of
CC   a reference sequence for PHKG2 protein or its fragment, where the
CC   reference sequence comprises a sequence (see ABB09290) of 406 amino
CC   acids, and the polymorphic variant comprises one or more variant amino
CC   acids selected from glutamic acid at a position corresponding to amino
CC   acid position 153 and tryptophan at position corresponding to amino acid
CC   position 329. (I) has hepatotropic activity and can be used in gene
CC   therapy. (II) is useful in screening for drugs targeting (II), by
CC   contacting a PHKG2 polymorphic variant with a candidate agent and
CC   assaying for binding activity. The identified candidate agents targeting
CC   PHKG2, are useful for treating liver cirrhosis and glycogen storage
CC   diseases. The present sequence represents a preferred oligonucleotide
CC   primer for the PHKG2 gene, which is used in the exemplification of the
CC   present invention
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGGAGGTGGG 10


RESULT 92
ABV78454/c
ID   ABV78454 standard; cDNA; 10 BP.
XX
AC   ABV78454;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human transcription factor CA150 SAGE tag, SEQ ID NO:165.
XX
KW   SAGE tag; serial analysis of gene expression; human; Th1 cell;
KW   activated T cell; T lymphocyte; immune response; expression pattern;
KW   preferential expression; immune disorder; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002186482-A.
XX
PD   02-JUL-2002.
XX
PF   19-DEC-2000; 2000JP-00385816.
XX
PR   19-DEC-2000; 2000JP-00385816.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-594261/64.
XX
PT   Human activated Th1 and Th2 cell expression gene group, useful for the
PT   diagnosis and treatment of Th1 and Th2-related diseases.
XX
PS   Claim 19; Page 11; 60pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are expressed in activated human Th1
CC   and/or Th2 cells. The SAGE tags of this invention consist of a sequence
CC   of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
CC   lying nearest to the polyA region of cDNAs derived from a variety of
CC   genes. These tags serve to uniquely identify each transcript and can thus
CC   be used to analyse the pattern of gene expression in particular cell
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CC   types. The invention also relates to proteins encoded by the genes
CC   expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
CC   inhibitors of the expression of groups of genes that are expressed in
CC   either or both the two cell types. Groups of genes expressed in Th1
CC   and/or Th2 cell types may be used for the diagnosis and treatment of Th1
CC   and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
CC   representing 171 genes which are more highly expressed in Th1 cells
CC   compared with Th2 cells
XX
SQ   Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
                 ||||| ||||
Db         10 TTCTGGCCAA 1


RESULT 93
ABV84246
ID   ABV84246 standard; cDNA; 10 BP.
XX
AC   ABV84246;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Human mitochondrial F0 complex ATP synthase-like EST SAGE tag #56.
XX
KW   SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
KW   CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
KW   expression pattern; differential expression; EST; expressed sequence tag;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   JP2002209591-A.
XX
PD   30-JUL-2002.
XX
PF   19-JAN-2001; 2001JP-00012328.
XX
PR   19-JAN-2001; 2001JP-00012328.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2002-631294/68.
XX
PT   Human chronic hepatitis C tissue expression exasperating gene group
PT   comprises 100 high-ranking genes.
XX
PS   Claim 1; Page 11; 139pp; Japanese.
XX
CC   The invention relates to SAGE (serial analysis of gene expression) tags
CC   representing groups of genes which are differentially expressed in human
CC   chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC   hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC   The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC   located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC   polyA region of cDNAs derived from a variety of genes. These tags serve
CC   to uniquely identify each transcript and can thus be used to analyse the
CC   pattern of gene expression in particular cell types. The invention also
CC   relates to proteins encoded by the genes expressed in chronic hepatitis C
CC   liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC   the expression of groups of genes that are overexpressed in chronic
CC   hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC   in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC   treatment of these diseases. Such genes, inhibitors of their expression
CC   or activity, and antibodies against the gene products may be used in the
CC   development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC   ABV84191-ABV84290 are SAGE tags representing the 100 most highly
CC   expressed genes out of those genes which are overexpressed in chronic
CC   hepatitis C liver tissue compared with normal liver tissue
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
                 || |||||||
Db          1 GCACAAGAAG 10


RESULT 94
ABK23703
ID   ABK23703 standard; DNA; 10 BP.
XX
AC   ABK23703;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #292 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 5 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
                 || |||||||
Db          1 GCACAAGAAG 10


RESULT 95
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ABN84506/c
ID ABN84506 standard; DNA; 10 BP.
XX
AC ABN84506;
XX
DT 21-OCT-2002 (first entry)
XX
DE Rat smooth muscle myosin heavy chain gene CArG2 motif.
XX
KW Smooth muscle; myosin; SM-MHC; rat; gene therapy; promoter; CArG2;
KW antiarteriosclerotic; antiasthmatic; antiinflammatory; cardiant;
KW hypotensive; transgenic animal; ds.
XX
OS Rattus sp.
XX
PN WO200259270-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002016.
XX
PR 24-JAN-2001; 2001US-0263811P.
XX
PA (OWEN/) OWENS G K.
PA (MANA/) MANABE I.
XX
PI Owens GK, Manabe I;
XX
DR WPI; 2002-599772/64.
XX
PT New smooth muscle myosin heavy chain promoter/enhancers, useful for
PT smooth muscle tissue-specific targeting and expression, or for genetic
PT engineering as a means to investigate smooth muscle cell physiology and
PT pathophysiology.
XX
PS Example 4; Page 56; 110pp; English.
XX
CC The present sequence is the CArG2 motif of the promoter/enhancer region
CC of the rat smooth muscle myosin heavy chain (SM-MHC) gene (see also
CC ABN84504). The present invention provides polynucleotide sequences which
CC confer to an operably linked polynucleotide cell-specific expression
CC within SM cells in vivo. These are derived from the rat or human SM-MHC
CC gene. In some, the CArG2 or the intron CArG motif is mutated to confer
CC subtype specificity. For example, the present sequence is preferably
CC altered to the sequence given in ABN84507 by site-directed mutagenesis.
CC The heterologous polynucleotide linked to the SM-MHC promoter preferably
CC encodes a toxin, a prodrug-converting enzyme, a tumour suppressor, a
CC sensitising agent, an apoptotic factor, an angiogenesis inhibitor, a
CC cytokine or an immunogenic antigen, or is an antisense polynucleotide or
CC a catalytic polynucleotide. Expression vectors, e.g. retroviral, adeno-
CC associated viral and adenoviral vectors, host cells and transgenic
CC animals are provided. The SM-MHC promoter/enhancer provides for specific
CC expression in SM cells of the bladder, gastrointestinal tract or urinary
CC tract, aorta artery, carotid artery, pulmonary artery, vena cava vein or
CC vascular SM. The compositions and methods for targeted gene delivery and
CC expression are useful in treating diseases associated with abnormal
CC function of SM cells, e.g. systemic hypertension, pulmonary hypertension,
CC atherosclerosis, asthma, coronary artery disease, gastrointestinal
CC abnormalities, reproductive dysfunction or chronic bronchitis
XX
SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1024 CCCAAGAAGG 1033
||||| ||||
Db 10 CCCAAAAAGG 1

RESULT 96
ACA60848/c
ID ACA60848 standard; DNA; 10 BP.
XX
AC ACA60848;
XX
DT 03-JUL-2003 (first entry)
XX
DE Rat smooth muscle myosin heavy chain wild-type CArG2 motif.
XX
KW Rat; ds; smooth muscle; myosin heavy chain; SM-MHC; CArG; hypotensive;
KW antiatherosclerotic; antiasthmatic; antiinflammatory; promoter; enhancer;
KW systemic hypertension; pulmonary hypertension; atherosclerosis; asthma;
KW coronary artery disease; gastrointestinal abnormality; stem cell;
KW reproductive dysfunction; chronic bronchitis; tissue regeneration.
XX
OS Rattus sp.
XX
PN US2003017549-A1.
XX
PD 23-JAN-2003.
XX
PF 24-JAN-2002; 2002US-00057726.
XX
PR 16-JAN-1998; 98US-0071300P.
PR 15-JAN-1999; 99WO-US001038.
PR 13-JUL-2000; 2000US-00600319.
PR 24-JAN-2001; 2001US-0263811P.
XX
PA (OWEN/) OWENS G K.
XX
PI Owens GK, Manabe I;
XX
DR WPI; 2002-599772/64.
XX
PT New smooth muscle myosin heavy chain promoter/enhancers, useful for
PT smooth muscle tissue-specific targeting and expression, or for genetic
PT engineering as a means to investigate smooth muscle cell physiology and
PT pathophysiology.
XX
PS Example 4; Page 23; 75pp; English.
XX
CC The invention relates to an isolated, synthetic, or recombinant
CC polynucleotide comprising a smooth muscle myosin heavy chain (SM-MHC)
CC promoter/enhancer sequence capable of conferring smooth muscle specific
CC expression in vivo. Also included are expression vectors comprising the
CC SM-MHC promoter/enhancers, a genetically engineered host cell comprising
CC the vector, a transgenic non-human animal comprising the SM-MHC promoter/
CC enhancer and screening a compound that modulates the activity of an SM-
CC MHC promoter/enhancer. The SM-MHC promoter/enhancer is useful for
CC expressing a polynucleotide (a reporter gene or polynucleotide encoding a
CC therapeutic protein) in a smooth muscle cell in vivo. The smooth muscle
CC cell is in a coronary artery, aorta, airway smooth muscle, or pulmonary
CC vascular smooth muscle, or bladder smooth muscle, gastrointestinal tract
CC smooth muscle, urinary tract smooth muscle, or gastrointestinal tract
CC smooth muscle, urinary tract smooth muscle, airway smooth muscle, vein
CC smooth muscle, or small branching artery smooth muscle. The SM-MHC
CC promoter/enhancer further comprises a minimal thymidine kinase (TK)
CC promoter. The targeted delivery of the SM-MHC promoter/enhancer is useful
CC for development of animal models of human disease to assist in
CC development of new therapeutic targets or development of animals models
CC for purpose of screening new drugs/therapies. The SM-MHC promoter/
CC enhancer facilitates targeted gene delivery to express a gene of interest
CC within an SMC. Targeted gene delivery and expression of the SM-MHC
CC promoter/enhancer is useful for treating diseases associated with
CC abnormal function of SMC including systemic hypertension, pulmonary
CC hypertension, atherosclerosis, asthma, coronary artery disease,
CC gastrointestinal abnormalities, reproductive dysfunction and chronic
CC bronchitis. The SM-MHC promoter/enhancer and transformed cells are useful
CC for identifying and selecting SMC derived from multi-potent stem cell
CC populations for purposes of tissue generation/regeneration for surgery
CC (e.g. for blood vessel, bladder, or gastrointestinal smooth muscle tissue
CC augmentation-reconstitution). The SM-MHC genes contain CArG motifs in
CC their promoter and first intron regions, these motifs are thought to be
CC responsible for smooth muscle cell subtype specific expression of SM-MHC.

```
CC   The present sequence is a rat SM-MHC wild-type CArG motif
XX
SQ   Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGAAGG 1033
                 ||||| ||||
Db         10 CCCAAAAAGG 1


RESULT 97
ABQ72900/c
ID   ABQ72900 standard; DNA; 10 BP.
XX
AC   ABQ72900;
XX
DT   06-SEP-2002  (first entry)
XX
DE   Human GRM8 gene polymorphism detection primer, SEQ ID NO:104.
XX
KW   Human; glutamate receptor metabotropic 8; GRM8; receptor;
KW   chromosome 7q31.3-32.1; neurotransmission; glutamate-mediated;
KW   Smith-Lemli-Opitz syndrome; retinitis pigmentosa;
KW   neuropathological disorder; neuroprotective; ophthalmological;
KW   gene therapy; haplotyping; genotyping; haplotype; genetic variant;
KW   single nucleotide polymorphism; SNP; drug screening; drug discovery;
KW   primer extension; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200238587-A2.
XX
PD   16-MAY-2002.
XX
PF   09-NOV-2001; 2001WO-US047325.
XX
PR   09-NOV-2000; 2000US-0247576P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bieglecki KM,  Chew A,  Choi JY,  Koshy B,  Parks KE;
XX
DR   WPI; 2002-519291/55.
XX
PT   Genetic variants of Glutamate Receptor, Metabotropic 8 isogenes, useful
PT   for improving efficiency and reliability in drug development for treating
PT   neuropathological conditions and retinitis pigmentosa.
XX
PS   Claim 17; Page 15; 110pp; English.
XX
CC   The invention relates to a method for haplotyping the glutamate receptor,
CC   metabotropic 8 (GRM8) gene (ABQ72798, ABQ72905) of an individual, and
CC   also describes 21 novel polymorphic sites within the human GRM8 gene. The
CC   GRM8 gene is located on chromosome 7q31.3-32.1 and contains 10 exons
CC   which encode a 908 amino acid protein (ABB09564). GRM8 is involved in
CC   glutamate-mediated neurotransmission, being a member of a subfamily of
CC   metabotropic glutamate receptors that inhibit the activity of adenylate
CC   cyclase in response to glutamate stimulation. The chromosomal location of
CC   the GRM8 gene encompasses regions linked to Smith-Lemli-Opitz syndrome
CC   and a form of retinitis pigmentosa. GRM8 nucleic acid sequences are
CC   useful in studying the expression and function of GRM8, and in expressing
CC   GRM8 protein for use in screening drugs for the treatment of GRM8-
CC   associated diseases (e.g., neuropathological disorders, Smith-Lemli-Opitz
CC   syndrome and retinitis pigmentosa). GRM8 nucleic acids and proteins are
CC   also useful in studying the effect of polymorphisms on the biological
CC   activity of GRM8. Polymorphisms in the target region may be determined by
CC   the use of allele-specific oligonucleotides (ASOs; ABQ72800-ABQ72862) as
CC   probes and primers, and by primer extension using oligonucleotide primers
CC   comprising sequences ABQ72863-ABQ72904. The method of the invention is
CC   useful for haplotyping the GRM8 gene in populations and in individuals,
CC   enabling decisions to be made as to whether GRM8 is a likely therapeutic
CC   target for a disease of interest, and in the design of clinical trials of
CC   candidate drugs for treating GRM8-associated disorders. In addition,
CC   transgenic animals comprising a human GRM8 gene are useful for studying
CC   the expression of GRM8 isogenes in vivo, for in vivo screening and
CC   testing of drugs targeted to GRM8, and for testing the efficacy of
CC   therapeutic agents and compounds for treating GRM8-associated conditions
CC   in a biological system. Sequences ABQ72863-ABQ72904 represent sequences
CC   that are specifically claimed as components of primers used to detect
CC   polymorphisms in the GRM8 gene by primer extension
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCCA 1027
                 |||||| |||
Db         10 CTTCTGACCA 1


RESULT 98
ABK96537/c
ID   ABK96537 standard; DNA; 10 BP.
XX
AC   ABK96537;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Human PLAU gene, primer extension primer 3' terminus #10.
XX
KW   Human; ss; primer; Plasminogen activator; urokinase; PLAU; cancer;
KW   cytostatic; serine protease; thrombolytic disorder; isogene; PCR;
KW   pulmonary embolism; chromosome 10q24-qter; haplotype; genotype; SNP;
KW   single nucleotide polymorphism; thrombolytic; gene therapy;
KW   primer extension.
XX
OS   Homo sapiens.
XX
PN   WO200240503-A2.
XX
PD   23-MAY-2002.
XX
PF   14-NOV-2001; 2001WO-US044001.
XX
PR   17-NOV-2000; 2000US-0249703P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Anastasio AE,  Bentivegna SC,  Koshy B;
XX
DR   WPI; 2002-519370/55.
XX
PT   Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes,
PT   useful for improving efficiency and reliability in drug development for
PT   treating thrombolytic disorders and cancer.
XX
PS   Claim 16; Page 14; 92pp; English.
XX
CC   The invention relates to a polynucleotide comprising a first nucleotide
CC   sequence (NS1) comprising a PLAU (plasminogen activator, urokinase, a
CC   serine protease) isogene selected from isogenes 1-9 and 11-20 given in
CC   the specification, where each isogene comprises the regions of the PLAU
CC   gene or cDNA and is further defined by the corresponding sequence of
CC   polymorphisms (defining single nucleotide polymorphisms, SNP). Also
CC   included are methods of haplotyping/genotyping (and predicting the
CC   haplotype/genotype of the PLAU gene of an individual, identifying an
CC   association between a trait and at least one haplotype or haplotype pair
CC   of the PLAU gene, an isolated oligonucleotide for detecting a
CC   polymorphism in the PLAU gene, a recombinant non-human organism
CC   transformed or transfected with the gene or cDNA, fragments of the
CC   polynucleotides of at least 10 base pairs encompassing a polymorphic
```

```
CC   site, an isolated polymorphic variant PLAU protein or fragment, an
CC   isolated monoclonal antibody specific for PLAU, a computer system for
CC   storing and analysing polymorphism data for the PLAU gene and a genome
CC   anthology for the PLAU gene. PLAU is useful in screening for drugs
CC   targeting PLAU that are useful for treating thrombolytic disorders and
CC   cancers. The methods are useful for improving the efficiency and
CC   reliability of the discovery and development of drugs for treating
CC   diseases associated with PLAU activity, in validating PLAU as a drug
CC   target and in the design of clinical trials for treating a specific
CC   condition of disease associated with PLAU activity. The antibody is
CC   useful in diagnostic, prognostic and therapeutic methods. PLAU
CC   polynucleotides are useful in studying the expression and function of
CC   PLAU, and in expressing PLAU protein for use in screening for candidate
CC   drugs to treat diseases related to PLAU activity. The gene for PLAU is
CC   located on chromosome 10q24-qter. The present sequence is the 3' terminus
CC   of an allele specific primer used to amplify PLAU polynucleotides with a
CC   specific polymorphism using the technique of primer extension
XX
SQ   Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              ||||||||| |
Db         10 TGCCCAAGGA 1


RESULT 99
ACF04526
ID   ACF04526 standard; DNA; 10 BP.
XX
AC   ACF04526;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Stuffer sequence used in NA detection by mass spectrometry #9.
XX
KW   Mass spectrometry; nucleic acid sequence detection; stuffer sequence; ds.
XX
OS   Synthetic.
XX
PN   WO2003060163-A2.
XX
PD   24-JUL-2003.
XX
PF   30-DEC-2002; 2002WO-NL000872.
XX
PR   28-DEC-2001; 2001EP-00205114.
XX
PA   (KEYG-) KEYGENE NV.
XX
PI   Van Eijk MJT,  Van Schaik C;
XX
DR   WPI; 2003-598543/56.
XX
PT   Determining the presence or absence of target sequences in nucleic acid
PT   samples, useful for e.g. genetic mapping or DNA fingerprinting, comprises
PT   employing an oligonucleotide ligation assay in combination with mass
PT   spectrometry.
XX
PS   Example 3; Page 27; 68pp; English.
XX
CC   The present invention relates to a method of determining the presence or
CC   absence of at least one target sequence in a nucleic acid sample, which
CC   comprises employing an oligonucleotide ligation assay in combination with
CC   a detection method based upon molecular mass, preferably mass
CC   spectrometry. The method is useful for high-throughput detection of a
CC   multiplicity of target nucleotide sequences, for detecting polymorphisms
CC   (preferably single nucleotide polymorphism), for transcript profiling,
CC   for detecting quantitative abundance of target nucleic acid sequences,
CC   for genetic mapping, gene discovery, marker-assisted selection, seed
CC   quality control, hybrid selection, QTL mapping, bulked segregant
CC   analysis, DNA fingerprinting and for disclosing information relating to
CC   traits, disease resistance, yield, hybrid vigor, and/or gene function.
CC   The set of oligonucleotide probes, which comprises a probe for each
CC   allele of a single nucleotide polymorphism, is useful for determining the
CC   presence or absence of at least one target sequence in a nucleic acid
CC   sample. The present sequence is a stuffer sequence used in the
CC   exemplification of the invention
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 100
ADI13685
ID   ADI13685 standard; DNA; 10 BP.
XX
AC   ADI13685;
XX
DT   22-APR-2004  (first entry)
XX
DE   Cytoplasmic tumour endothelial marker standard tag SEQ ID NO:60.
XX
KW   tumour endothelial marker; TEM; endothelial cell regulation;
KW   neoangiogenesis inhibition; neoangiogenesis screening;
KW   neoangiogenesis promotion; neoangiogenesis; tumour; wound healing;
KW   cytostatic; vulnerary; human; standard tag; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004005883-A2.
XX
PD   15-JAN-2004.
XX
PF   02-JUL-2003; 2003WO-US016250.
XX
PR   02-JUL-2002; 2002US-0393023P.
PR   01-APR-2003; 2003US-0458964P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   St Croix B,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2004-142995/14.
XX
PT   Use of tumor endothelial marker proteins for inhibiting neoangiogenesis,
PT   screening for neoangiogenesis, promoting neoangiogenesis, identifying
PT   candidate drugs for treating tumors or promoting wound healing.
XX
PS   Disclosure; SEQ ID NO 60; 113pp; English.
XX
CC   The present invention describes the use of tumour endothelial marker
CC   (TEM) proteins for identifying a ligand involved in endothelial cell
CC   regulation, inhibiting neoangiogenesis, screening for neoangiogenesis,
CC   promoting neoangiogenesis, identifying candidate drugs for treating
CC   tumours or promoting wound healing or identifying endothelial cells. Also
CC   described: (1) identification of a ligand involved in endothelial cell
CC   regulation; (2) inhibiting neoangiogenesis; (3) promoting neoangiogenesis
CC   in a patient; (4) screening for neoangiogenesis in a patient; (5)
CC   identify candidate drugs for treating tumours or promoting wound healing;
CC   and (6) identifying endothelial cells. TEM proteins have cytostatic and
CC   vulnerary activities. The TEM proteins are useful for identifying a
CC   ligand involved in endothelial cell regulation, inhibiting
CC   neoangiogenesis, screening for neoangiogenesis, promoting
CC   neoangiogenesis, identifying candidate drugs for treating tumours or
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CC   promoting wound healing or identifying endothelial cells. The present
CC   sequence represents a cytoplasmic tumour endothelial marker standard tag
CC   oligonucleotide, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 101
ADM69071
ID   ADM69071 standard; DNA; 10 BP.
XX
AC   ADM69071;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human TAT protein-related tag ASCL2 oligonucleotide SeqID7.
XX
KW   achaete-scute like-2; tumour-associated antigenic target polypeptide;
KW   TAT376; TAT377; TAT; cytostatic; gene therapy;
KW   cell proliferative disorder; tumour; cancer; prostate cancer;
KW   lung cancer; breast cancer; colon cancer; ovarian cancer;
KW   chromosome mapping; gene mapping; tissue typing; ASCL-2; ss; human.
XX
OS   Homo sapiens.
XX
PN   WO2004019857-A2.
XX
PD   11-MAR-2004.
XX
PF   04-JUN-2003; 2003WO-US017682.
XX
PR   29-AUG-2002; 2002US-0407087P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baldwin D,  Clark H,  Jubb A,  Koeppen H,  Quan C,  Wu TD,  Zhang Z;
XX
DR   WPI; 2004-239106/22.
XX
PT   New TAT376 and TAT377 nucleic acid, useful for preparing a medicament for
PT   treating or diagnosing a cell proliferative disorder, tumor or cancer,
PT   e.g. prostate, lung, breast, colon or ovarian cancer.
XX
PS   Example 2; SEQ ID NO 7; 159pp; English.
XX
CC   This invention relates to novel isolated nucleic acids and their encoded
CC   achaete-scute like-2 polypeptides. In particular, the invention relates
CC   to tumour-associated antigenic target polypeptides (TAT) 376 and 377 and
CC   the DNA sequences which encode them. The invention may be useful for the
CC   development of compounds with a cytostatic activity or for gene therapy.
CC   TAT376 or TAT377 nucleic acids, polypeptides, antibodies or oligopeptides
CC   are useful for preparing a medicament for treating or diagnosing a cell
CC   proliferative disorder, tumour or cancer (for example prostate, lung,
CC   breast, colon or ovarian cancer). The nucleic acids may be used as
CC   hybridisation probes for a cDNA library to isolate the full length TAT376
CC   or TAT377 cDNA, in chromosome or gene mapping, in gene therapy, and in
CC   tissue typing. The present sequence is that of an oligonucleotide which
CC   was used in the exemplification of the invention.
XX
SQ   Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              ||| ||||||
Db          1 CTGGCCAAGA 10


RESULT 102
ADM33249/c
ID   ADM33249 standard; DNA; 10 BP.
XX
AC   ADM33249;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Oligo SEQ ID 84, used in method for estimating melting temperature.
XX
KW   Melting temperature; probe design; primer design; ss.
XX
OS   Synthetic.
XX
PN   WO2004025257-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028664.
XX
PR   12-SEP-2002; 2002US-0410663P.
XX
PA   (INTE-) INTEGRATED DNA TECHNOLOGIES INC.
XX
PI   Owczarzy R,  Walder JA,  Huang L,  Behlke MA;
XX
DR   WPI; 2004-340203/31.
XX
PT   Estimating melting temperature, for designing or selecting
PT   oligonucleotide probes or primers, comprises modifying the reference
PT   melting temperature by a logarithm of the ratio of the desired ion to the
PT   reference ion concentrations.
XX
PS   Example 1; Page 41; 66pp; English.
XX
CC   The present invention relates to a method for estimating a melting
CC   temperature (Tm) for a polynucleotide at a desired ion concentration
CC   having a known G-C content value. The method is useful designing and
CC   selecting oligonucleotide probes and primers. The present sequence was
CC   used to illustrate the method of the invention.
XX
SQ   Sequence 10 BP; 2 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 53;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              |||||| |||
Db         10 AAGAAGTTGG 1


RESULT 103
AAA16595
ID   AAA16595 standard; DNA; 11 BP.
XX
AC   AAA16595;
XX
DT   16-JUN-2000  (first entry)
XX
DE   Human MN gene 5' donor consensus splice sequence SEQ ID NO:73.
XX
KW   Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW   oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW   MN/CA IX isoenzyme; ds.
XX
OS   Homo sapiens.
```

```
XX
PN   US6027887-A.
XX
PD   22-FEB-2000.
XX
PF   24-JAN-1997;   97US-00787739.
XX
PR   21-OCT-1992;   92US-00964589.
PR   30-DEC-1993;   93US-00177093.
PR   15-JUN-1994;   94US-00260190.
PR   07-JUN-1995;   95US-00477504.
PR   07-JUN-1995;   95US-00481658.
PR   07-JUN-1995;   95US-00485049.
PR   07-JUN-1995;   95US-00485862.
PR   07-JUN-1995;   95US-00485863.
PR   07-JUN-1995;   95US-00486756.
PR   07-JUN-1995;   95US-00487077.
XX
PA   (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI   Pastorek J,  Zavada J,  Pastorekova S;
XX
DR   WPI; 2000-194827/17.
XX
PT   Nucleic acid based assay for diagnosing a wide variety of
PT   preneoplastic/neoplastic disease comprises screening for the presence of
PT   abnormal MN gene expression in a vertebrate.
XX
PS   Disclosure; Col 16; 87pp; English.
XX
CC   The present invention describes a method of screening for
CC   preneoplastic/neoplastic disease. The method comprises: (1) determining
CC   whether abnormal MN gene expression is present in a vertebrate; and (2)
CC   if abnormal MN gene expression is determined to be present in the
CC   vertebrate, determining that the vertebrate has a significant risk of
CC   having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC   encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC   protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC   is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC   in a vertebrate, preferably a human. The disease detected is mammary,
CC   bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC   vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC   testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC   duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC   mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC   mucosa, pancreatic duct epithelium or liver duct epithelium
CC   preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC   AAY53245 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 104
AAA52514
ID   AAA52514 standard; DNA; 11 BP.
XX
AC   AAA52514;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Human MN gene intron 7 splice donor sequence.
XX
KW   MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW   proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW   abnormal expression; neoplastic disease; cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200024913-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-US024879.
XX
PR   23-OCT-1998;   98US-00177776.
PR   23-OCT-1998;   98US-00178115.
XX
PA   (FARB ) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J,  Pastorekova S,  Pastorek J;
XX
DR   WPI; 2000-350752/30.
XX
PT   A molecule which specifically binds to a site on MN protein (oncoprotein)
PT   and prevents adhesion of vertebrate cells to the protein, useful for
PT   treating preneoplastic or neoplastic diseases such as cancer.
XX
PS   Disclosure; Page 26; 154pp; English.
XX
CC   The invention relates to the inhibition of cell adhesion mediated by the
CC   MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC   protein). The MN protein is a tumour-associated adhesion molecule which
CC   comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC   protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC   Abnormal expression of the MN protein is associated with tumorigenicity.
CC   The invention encompasses molecules (e.g., proteins and peptides) which
CC   which specifically bind to a site on the MN protein, thereby preventing
CC   adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC   also encompasses MN proteins or MN protein fragments which can be added
CC   to the extracellular environment to prevent the adhesion of vertebrate
CC   cells to each other. The invention also relates to the identification of
CC   the binding site of the MN protein and to a method of identifying a site
CC   on an MN protein to which cells adhere, comprising testing a series of
CC   overlapping peptides from the protein in a cell adhesion assay. The
CC   invention encompasses a vector comprising an expression control sequence
CC   operatively linked to a nucleic acid encoding the variable domains of a
CC   MN-specific antibody, where the domains are separated by a flexible
CC   linker peptide (AAB03035) and the vector inhibits the growth of a
CC   vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC   protein. The invention also encompasses a vector comprising a nucleic
CC   acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC   gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC   neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC   gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC   and peptides, and expression vectors encoding such proteins and peptides
CC   are useful for treating patients with preneoplastic or neoplastic disease
CC   (e.g., cancers) associated with or characterised by abnormal MN
CC   expression. The present sequence represents a fragment of the human MN
CC   gene (AAA52462) specified in the invention
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 105
ABQ87504/c
ID   ABQ87504 standard; cDNA; 11 BP.
XX
AC   ABQ87504;
```

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XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1259.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 89; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              ||| ||||||
Db         11 CAATAAGGTG 2


RESULT 106
ABQ87500/c
ID   ABQ87500 standard; cDNA; 11 BP.
XX
AC   ABQ87500;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 1255.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 89; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 107
ABQ86415
ID   ABQ86415 standard; cDNA; 11 BP.
XX
AC   ABQ86415;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Human skin stress/ageing related EST SEQ ID NO 170.
XX
KW   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253773-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015178.
XX
PR   03-JAN-2001; 2001DE-01000121.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-528865/56.
XX
PT   Identifying genes involved in skin stress and aging, useful e.g. in
PT   screening for cosmetic or therapeutic agents, based on differential gene
PT   expression.
XX
PS   Claim 8; Page 44; 325pp; German.
XX
CC   The invention relates to identifying (M1) genes in vitro that, in humans
CC   or animals, are important for skin ageing and/or skin stress by serial
CC   analysis of gene expression between mixtures of transcribed and
```

```
CC   optionally translated, genetically encoded factors (A) obtained from
CC   young and aged skin, to identify that genes that show strong differential
CC   expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC   useful for: identifying markers of skin ageing and/or stress; determining
CC   skin ageing and/or stress; and identifying or determining the effects of
CC   pharmaceutical or cosmetic agents for control of skin ageing. The present
CC   sequence is one of a group of human skin ageing/stress related expressed
CC   sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ   Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 108
ABV66344
ID   ABV66344 standard; cDNA; 11 BP.
XX
AC   ABV66344;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4130.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 139; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              ||||||| ||
Db          2 TGCCCAAAAA 11


RESULT 109
ABV62764
ID   ABV62764 standard; cDNA; 11 BP.
XX
AC   ABV62764;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 550.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 40; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db          1 AAGGAGGTGG 10


RESULT 110
ABV70185
ID   ABV70185 standard; cDNA; 11 BP.
XX
AC   ABV70185;
XX
```

DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7971.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 254; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
                ||| ||||||
Db          1 AAGGAGGTGG 10
```

RESULT 111
ABV62651/c
ID ABV62651 standard; cDNA; 11 BP.
XX
AC ABV62651;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 437.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 37; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
                ||||||  |||
Db         11 AGAAGGCGGG 2
```

RESULT 112
ABV67006
ID ABV67006 standard; cDNA; 11 BP.
XX
AC ABV67006;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 4792.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against

```
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 157; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 113
ABV67047/c
ID   ABV67047 standard; cDNA; 11 BP.
XX
AC   ABV67047;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4833.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 158; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 114
ABV64836
ID   ABV64836 standard; cDNA; 11 BP.
XX
AC   ABV64836;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 2622.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 98; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              || |||||||
Db          1 AAAAAGGTGG 10
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RESULT 115
ABV67092/c
ID   ABV67092 standard; cDNA; 11 BP.
XX
AC   ABV67092;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 4878.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 159; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db         10 AAGCAGGTGG 1


RESULT 116
ABV67518/c
ID   ABV67518 standard; cDNA; 11 BP.
XX
AC   ABV67518;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5304.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 171; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
              |||| |||||
Db         11 TTCTACCCAA 2


RESULT 117
ABV72108/c
ID   ABV72108 standard; cDNA; 11 BP.
XX
AC   ABV72108;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 9894.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
```

PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 323; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1020 TCTGCCCAAG 1029
|||||||||
Db 11 TGTGCCCAAG 2

RESULT 118
ABV62632
ID ABV62632 standard; cDNA; 11 BP.
XX
AC ABV62632;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 418.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 37; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1026 CAAGAAGGTG 1035
||||||.|||
Db 2 CAAGAAAGTG 11

RESULT 119
ABV65381
ID ABV65381 standard; cDNA; 11 BP.
XX
AC ABV65381;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 3167.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 113; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 3 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

```
  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
             ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 120
ABV67446/c
ID   ABV67446 standard; cDNA; 11 BP.
XX
AC   ABV67446;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 5232.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 169; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
             ||| ||||||
Db         11 CAATAAGGTG 2


RESULT 121
ABV66204/c
ID   ABV66204 standard; cDNA; 11 BP.
XX
AC   ABV66204;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3990.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Disclosure; Page 135; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
             | ||||||||
Db         10 TCCTGCCCAA 1


RESULT 122
ABV65314/c
ID   ABV65314 standard; cDNA; 11 BP.
XX
AC   ABV65314;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 3100.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
```

PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 111; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1028 AGAAGGTGGG 1037
|||| |||||
Db 11 AGAAAGTGGG 2

RESULT 123
ABV70072/c
ID ABV70072 standard; cDNA; 11 BP.
XX
AC ABV70072;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7858.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 250; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1028 AGAAGGTGGG 1037
|||||| |||
Db 11 AGAAGGCGGG 2

RESULT 124
ABV69202
ID ABV69202 standard; cDNA; 11 BP.
XX
AC ABV69202;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 6988.
XX
KW Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 219; 1345pp; German.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or

```
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 6 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 125
ABV70053
ID   ABV70053 standard; cDNA; 11 BP.
XX
AC   ABV70053;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Human skin EST 7839.
XX
KW   Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
KW   immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW   psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS   Homo sapiens.
XX
PN   WO200253774-A2.
XX
PD   11-JUL-2002.
XX
PF   20-DEC-2001; 2001WO-EP015179.
XX
PR   03-JAN-2001; 2001DE-01000127.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Conradt M,  Hofmann K;
XX
DR   WPI; 2002-590638/63.
XX
PT   In vitro identification of skin-expressed genes, useful for determining
PT   homeostasis and identifying cosmetic or pharmaceutical agents against
PT   e.g. skin cancer.
XX
PS   Claim 24; Page 250; 1345pp; German.
XX
CC   The invention relates to in vitro identification (M1) of genes expressed
CC   in the skin of humans or animals by subjecting a mixture of genetically
CC   encoded factors from skin, to serial analysis of gene expression (SAGE)
CC   so as to identify skin-expressed genes and quantify their expression.
CC   (M1) is useful for identifying genes involved in skin homeostasis; to
CC   determine skin homeostasis and to test agent (A) that maintains or
CC   promotes skin homeostasis or that can be used for treating skin
CC   disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC   ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC   rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC   skin. The present sequence is that of a human expressed sequence tag
CC   (EST) of the invention
XX
SQ   Sequence 11 BP; 5 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              |||||| |||
Db          2 CAAGAAAGTG 11


RESULT 126
ADG88256/c
ID   ADG88256 standard; DNA; 11 BP.
XX
AC   ADG88256;
XX
DT   22-APR-2004  (first entry)
XX
DE   A. thaliana pathogen infection-related gene motif 2 cis element #698.
XX
KW   Pathogen infection-related gene; plant; Peronospora parasitica;
KW   defence mechanism; pathogen resistance; transgenic plant; oomycete;
KW   fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;
KW   motif 2; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200222675-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028506.
XX
PR   15-SEP-2000; 2000US-0232778P.
PR   22-JUN-2001; 2001US-0300183P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYNC-) UNIV NORTH CAROLINA.
PA   (GLAZ/) GLAZEBROOK J.
PA   (WANG/) WANG X.
PA   (DANG/) DANGL J L.
PA   (EULG/) EULGEM T.
PA   (ZHUT/) ZHU T.
XX
PI   Glazebrook J,  Wang X,  Dangl JL,  Eulgem T,  Zhu T;
XX
DR   WPI; 2002-292409/33.
XX
PT   Novel isolated polynucleotide, useful for conveying pathogen resistance
PT   to plants, and for identifying plants infected with a pathogen.
XX
PS   Claim 44; SEQ ID NO 698; 605pp; English.
XX
CC   The invention relates to 691 Arabidopsis thaliana genes (ADG87559--
CC   ADG87557}) whose expression is altered in response to pathogen infection,
CC   and to homologues of these genes from other plants or fungi, especially
CC   from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
CC   cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The
CC   expression of genes of the invention was upregulated or downregulated in
CC   Arabidopsis plants infected with the oomycete Peronospora parasitica,
CC   indicating that they play a role in defence mechanisms. The genes of the
CC   invention are regulated by RPP7 or RRP8 which act via unconventional
CC   signalling cascades, or by the RPP4-dependent pathway. The invention also
CC   relates to polypeptides encoded by the pathogen infection-related genes;
CC   promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)
CC   ; expression cassettes, host cells and pathogen-resistant transgenic
CC   plants and their progeny comprising a polynucleotide of the invention;
CC   and a method of identifying a plant cell infected with a pathogen. The
CC   polynucleotide sequences and methods of the invention are useful for
CC   identifying plants infected with a pathogen, and for conferring
CC   resistance to pathogens such as oomycetes, fungi, bacteria, viruses,
CC   neamotodes and insects (e.g., aphids). The present sequence represents a
CC   cis element from the promoter of Arabidopsis thaliana gene whose
CC   expression is altered in response to Peronospora parasitica infection.
CC   Note: The sequence data for this patent can also be obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
```

```
SQ   Sequence 11 BP; 4 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCAA 1028
              || |||||||
Db         11 TTTTGCCCAA 2


RESULT 127
ADK41823
ID   ADK41823 standard; DNA; 11 BP.
XX
AC   ADK41823;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human MN gene intron-exon boundary sequence SeqID52.
XX
KW   carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
KW   human; vertebrate; cytostatic; vaccine; gene therapy;
KW   renal cell carcinoma; breast cancer; colorectal cancer; splice acceptor;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2004005348-A1.
XX
PD   15-JAN-2004.
XX
PF   22-FEB-2003; 2003WO-US005137.
XX
PR   23-MAY-2002; 2002US-0383068P.
PR   05-DEC-2002; 2002US-0431499P.
XX
PA   (FARB ) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J,  Pastorekova S,  Pastorek J,  Zavadova Z;
XX
DR   WPI; 2004-083500/08.
XX
PT   New soluble form of the carbonic anhydrase IX (CA IX) protein for
PT   screening, diagnosing or prognosing diseases associated with abnormal
PT   expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
PT   colorectal cancer.
XX
PS   Disclosure; SEQ ID NO 52; 159pp; English.
XX
CC   This invention relates to a novel soluble form of the carbonic anhydrase
CC   IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
CC   precancerous and/or cancerous cells of a vertebrate into a body fluid.
CC   The invention may be useful for the development of compounds with a
CC   cytostatic activity or a vaccine whilst the disclosed sequences may be
CC   used for gene therapy. The protein and method are useful for screening,
CC   diagnosing or prognosing diseases associated with abnormal expression of
CC   carbonic anhydrase IX protein, such as precancerous and cancerous
CC   diseases like renal cell carcinoma, breast cancer or colorectal cancer.
CC   The monoclonal antibody may also be used for treating or preventing
CC   precancerous and cancerous diseases. The present sequence is that of a
CC   splice acceptor site from a human MN gene intron-exon boundary which is
CC   related to the invention.
XX
SQ   Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db         1 AGCAGGTGGG 10


RESULT 128
ADQ35643/c
ID   ADQ35643 standard; DNA; 11 BP.
XX
AC   ADQ35643;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human hair-bearing skin-associated DNA fragment SEQ ID NO 460.
XX
KW   hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260931-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060931.
XX
PR   20-DEC-2002; 2002DE-01060931.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518857/50.
XX
PT   In vitro identification of genes important for hair-bearing skin, useful
PT   for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 460; 250pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for hair-bearing skin in humans. The method
CC   comprises recovering, from hair-bearing skin, a first mixture of
CC   genetically expressed (transcribed and optionally translated) factors
CC   (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC   mixture from skin on which hair does not grow and subjecting both
CC   mixtures to serial analysis of gene expression (SAGE) to identify those
CC   genes for which expression is markedly different between the two types of
CC   skin. The invention also describes in vitro methods for determining
CC   homeostasis of human hair-bearing skin and for determining activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC   a test kit comprising a solid support (flexible or rigid) with
CC   immobilised probes are also described for determining homeostasis. The
CC   hair-bearing skin is from the scalp and the other skin is from the face.
CC   The method allows identification of as many as possible of the genes
CC   important for hair-bearing skin, and therefore, of a very wide range of
CC   potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC   human DNA Tag fragments used to identify genes associated with hair-
CC   bearing skin.
XX
SQ   Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 129
ADQ35785/c
```

```
ID   ADQ35785 standard; DNA; 11 BP.
XX
AC   ADQ35785;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human hair-bearing skin-associated DNA fragment SEQ ID NO 602.
XX
KW   hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260931-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060931.
XX
PR   20-DEC-2002; 2002DE-01060931.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518857/50.
XX
PT   In vitro identification of genes important for hair-bearing skin, useful
PT   for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 5; SEQ ID NO 602; 250pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for hair-bearing skin in humans. The method
CC   comprises recovering, from hair-bearing skin, a first mixture of
CC   genetically expressed (transcribed and optionally translated) factors
CC   (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC   mixture from skin on which hair does not grow and subjecting both
CC   mixtures to serial analysis of gene expression (SAGE) to identify those
CC   genes for which expression is markedly different between the two types of
CC   skin. The invention also describes in vitro methods for determining
CC   homeostasis of human hair-bearing skin and for determining activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC   a test kit comprising a solid support (flexible or rigid) with
CC   immobilised probes are also described for determining homeostasis. The
CC   hair-bearing skin is from the scalp and the other skin is from the face.
CC   The method allows identification of as many as possible of the genes
CC   important for hair-bearing skin, and therefore, of a very wide range of
CC   potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC   human DNA Tag fragments used to identify genes associated with hair-
CC   bearing skin.
XX
SQ   Sequence 11 BP; 1 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
             |||||||| |
Db         10 CTGCCCAAAA 1


RESULT 130
ADQ34760/c
ID   ADQ34760 standard; DNA; 11 BP.
XX
AC   ADQ34760;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 2850.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
KW   homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS   Homo sapiens.
XX
PN   DE10260928-A1.
XX
PD   08-JUL-2004.
XX
PF   20-DEC-2002; 2002DE-01060928.
XX
PR   20-DEC-2002; 2002DE-01060928.
XX
PA   (HENK ) HENKEL KGAA.
XX
PI   Petersohn D,  Schlotmann K,  Gassenmeier T,  Holtkoetter O;
PI   Conradt M,  Hofmann K;
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 4; SEQ ID NO 2850; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
             ||| ||||||
Db         10 AAGCAGGTGG 1


RESULT 131
ADQ32076
ID   ADQ32076 standard; DNA; 11 BP.
XX
AC   ADQ32076;
XX
DT   23-SEP-2004  (first entry)
XX
DE   Human facial skin-associated DNA fragment SEQ ID NO 166.
XX
KW   facial skin; human; serial analysis of gene expression; SAGE;
```

KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 9; SEQ ID NO 166; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 6 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10
```

RESULT 132
ADQ34356/c
ID ADQ34356 standard; DNA; 11 BP.
XX
AC ADQ34356;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 2446.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 4; SEQ ID NO 2446; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 2 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1028 AGAAGGTGGG 1037
              |||| |||||
Db         11 AGAAAGTGGG 2
```

RESULT 133
ADQ34361
ID ADQ34361 standard; DNA; 11 BP.
XX
AC ADQ34361;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 2451.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX

PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 4; SEQ ID NO 2451; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 4 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1023 GCCCAAGAAG 1032
||||| ||||
Db 2 GCCCAGGAAG 11

RESULT 134
ADQ33229
ID ADQ33229 standard; DNA; 11 BP.
XX
AC ADQ33229;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 1319.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518855/50.
XX
PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 1319; 577pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX
SQ Sequence 11 BP; 4 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 42.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1021 CTGCCCAAGA 1030
||||| ||||
Db 2 CTGCCAAAGA 11

RESULT 135
ADQ32097
ID ADQ32097 standard; DNA; 11 BP.
XX
AC ADQ32097;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human facial skin-associated DNA fragment SEQ ID NO 187.
XX
KW facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
PN DE10260928-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060928.
XX
PR 20-DEC-2002; 2002DE-01060928.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;

```
XX
DR   WPI; 2004-518855/50.
XX
PT   In vitro identification of genes important for facial skin, useful for
PT   assessing homeostasis and in screening for pharmaceutical or cosmetic
PT   agents, based on differential expression analysis.
XX
PS   Claim 9; SEQ ID NO 187; 577pp; German.
XX
CC   This invention describes a novel in vitro method for identifying genes
CC   that are significant for facial skin in humans. The method comprises
CC   recovering, from facial skin, a first mixture of genetically expressed
CC   (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC   their fragments), recovering a second, similar mixture from some other
CC   human tissue, preferably skin from a protected area, especially from the
CC   breast and subjecting the mixtures to serial analysis of gene expression
CC   (SAGE) to identify those genes for which expression is markedly different
CC   between facial skin and the other tissue. The invention also describes an
CC   in vitro method for determining homeostasis of human facial skin; a test
CC   kit which comprises a solid support (flexible or rigid) on which are
CC   immobilised probes that bind specifically to the factors of interest and
CC   a biochip for determining homeostasis of human facial skin. The products
CC   of the invention are also used in a method which determines activity of
CC   cosmetic and pharmaceutical agents for use against disorders or
CC   disturbances of the homeostasis of human skin and a screening method for
CC   identifying cosmetic and pharmaceutical agents. The method allows
CC   identification of as many as possible of the genes important for facial
CC   skin and thus of a very wide range of potential therapeutic and cosmetic
CC   agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC   identify the facial skin-associated genes described in the invention.
XX
SQ   Sequence 11 BP; 6 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

  Query Match            42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity  90.0%;  Pred. No. 58;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 136
AAT09397
ID   AAT09397 standard; DNA; 8 BP.
XX
AC   AAT09397;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 4 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match            40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 4.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
              ||||||||
Db          1 CAAGAAGG 8


RESULT 137
AAT09546/c
ID   AAT09546 standard; DNA; 8 BP.
XX
AC   AAT09546;
XX
DT   25-MAR-2003  (revised)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
```

```
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 0 A; 3 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
             ||||||||
Db          8 CAAGAAGG 1


RESULT 138
AAT09415
ID   AAT09415 standard; DNA; 8 BP.
XX
AC   AAT09415;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1996  (first entry)
XX
DE   5'-primer used for characterisation of human biological samples.
XX
KW   5'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Claim 5; Page 44; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 4 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAG 1032
             ||||||||
Db          1 CCAAGAAG 8


RESULT 139
AAT09568/c
ID   AAT09568 standard; DNA; 8 BP.
XX
AC   AAT09568;
XX
DT   25-MAR-2003  (revised)
DT   25-JUN-1996  (first entry)
XX
DE   3'-primer used for characterisation of human biological samples.
XX
KW   3'-primer; human; protein coding region; PCR primer kit;
KW   characterisation; biological samples; PCR amplification; indexing;
KW   identification; cloning; analysis; genes; genome mapping;
KW   disease diagnosis; ss.
XX
OS   Synthetic.
XX
PN   WO9531574-A1.
XX
PD   23-NOV-1995.
XX
PF   12-MAY-1995;   95WO-US006032.
XX
PR   16-MAY-1994;   94US-00242887.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
PI   Lopeznieto CE,  Nigam SK;
XX
DR   WPI; 1996-010958/01.
XX
PT   Characterisation of nucleotide sequences using primer pairs - by PCR
PT   amplification and indexing of amplification prods. w.r.t. primers used
PT   for genome mapping and disease diagnosis.
XX
PS   Disclosure; Page 19; 72pp; English.
XX
CC   The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
CC   target human protein coding regions, together comprise a PCR primer kit
CC   with 1361 possible primer pairs. The kit is used in a new method for the
CC   characterisation of nucleic acid sequences obtd. from human biological
CC   samples, which comprises PCR amplification and indexing of the prods.
CC   w.r.t the primer pair that hybridised to its delineating subsequences.
CC   The method may be used in the identification, cloning and analysis of
CC   genes, e.g. in genome mapping, and disease diagnosis. (Updated on 25-MAR-
CC   2003 to correct PI field.)
XX
SQ   Sequence 8 BP; 0 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAG 1032
             ||||||||
Db          8 CCAAGAAG 1


RESULT 140
ABQ71965
ID   ABQ71965 standard; DNA; 9 BP.
XX
AC   ABQ71965;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2263.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
```

```
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 59; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 141
ABQ71964
ID   ABQ71964 standard; DNA; 9 BP.
XX
AC   ABQ71964;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2262.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 59; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 142
ABQ71781
ID   ABQ71781 standard; DNA; 9 BP.
XX
AC   ABQ71781;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2079.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
```

```
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 55; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          1 AAGGTGGG 8


RESULT 143
ABQ71780
ID   ABQ71780 standard; DNA; 9 BP.
XX
AC   ABQ71780;
XX
DT   28-AUG-2002  (first entry)
XX
DE   Zinc finger protein related oligonucleotide target SEQ ID NO:2078.
XX
KW   Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200242459-A2.
XX
PD   30-MAY-2002.
XX
PF   20-NOV-2001; 2001WO-US043438.
XX
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Liu Q;
XX
DR   WPI; 2002-500284/53.
XX
PT   New zinc finger protein that binds to target site, useful in studying
PT   gene function and for human therapeutics and plant engineering, comprises
PT   first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS   Example 1; Page 55; 81pp; English.
XX
CC   The present invention describes a zinc finger protein (I) that binds to a
CC   target site, comprising a first (F1), a second (F2), and a third (F3)
CC   zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC   target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC   and a third (S3) target subsite. Also described are: (1) a polypeptide
CC   (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC   (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC   binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC   binds to the S2 target subsite, and selecting the F3 zinc finger such
CC   that it binds to the S3 target subsite, thus designing (I) that binds to
CC   a target site. (I) is useful for recognition of triplet target subsites
CC   having the nucleotide G in the 5'-most position of the subsite. (I) is
CC   useful in studying gene function, and for human therapeutics and plant
CC   engineering. (I), (II) or (III) is useful in therapeutic methods to
CC   modulate the expression of a target region within a subject, in
CC   diagnostic methods for sequence specific detection of target nucleic acid
CC   in a sample, and in assays to determined the phenotype and function of
CC   gene expression. (I) has improved affinity and specificity for their
CC   target sequences, as well as enhanced biological activity. ABQ71213 to
CC   ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC   finger peptides which are given in the exemplification of the present
CC   invention
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          1 AAGGTGGG 8


RESULT 144
ACD06034/c
ID   ACD06034 standard; DNA; 9 BP.
XX
AC   ACD06034;
XX
DT   05-AUG-2003  (first entry)
XX
DE   Human VEGF-targeted zinc finger protein target sequence #7.
XX
KW   Zinc finger protein; antiarteriosclerotic; vasotropic; antiarthritic;
KW   cytostatic; antipsoriatic; ophthalmological; antidiabetic; antiulcer;
KW   vulnerary; gene therapy; vascular endothelial growth factor; VEGF;
KW   angiogenesis; atherosclerosis; ischaemia; arthritis; tumour; psoriasis;
KW   diabetic retinopathy; ulcer; wound; ds.
XX
OS   Homo sapiens.
XX
PN   US2003044404-A1.
XX
PD   06-MAR-2003.
XX
PF   30-APR-2001; 2001US-00846033.
XX
PR   07-DEC-2000; 2000US-00733604.
PR   12-DEC-2000; 2000US-00736083.
XX
PA   (REBA/) REBAR E.
PA   (JAMI/) JAMIESON A.
PA   (LIUQ/) LIU Q.
```

PA (LIUP/) LIU P.
PA (WOLF/) WOLFFE A.
PA (EISE/) EISENBERG S P.
PA (JARV/) JARVIS E.
XX
PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;
PI Jarvis E;
XX
DR WPI; 2003-456550/43.
XX
PT New zinc finger protein that binds to a target site in the human vascular
PT endothelial growth factor gene, useful for regulating angiogenesis, e.g.
PT in the treatment of atherosclerosis, ischemia, arthritis, tumors, ulcer
PT or wounds.
XX
PS Example 6; Page 42; 75pp; English.
XX
CC The invention describes a zinc finger protein (ZFP) that binds to a
CC target site having a nucleotide sequence of any of the human vascular
CC endothelial growth factor (VEGF) genes listed in the specification. The
CC composition and methods are useful in regulating angiogenesis, such as in
CC the treatment of atherosclerosis, ischaemia, arthritis, tumours,
CC psoriasis, diabetic retinopathy, ulcer or wounds. The composition may
CC also be used in screening for agents capable of modulating angiogenesis,
CC and in various diagnostic applications. This sequence represents a
CC vascular endothelial growth factor (VEGF) targeting zinc finger protein
CC zinc finger domain target DNA
XX
SQ Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1020 TCTGCCCA 1027
||||||||
Db 8 TCTGCCCA 1

RESULT 145
ACD19256/c
ID ACD19256 standard; DNA; 9 BP.
XX
AC ACD19256;
XX
DT 22-AUG-2003 (first entry)
XX
DE Human VEGF-targeted ZFP HUM 19A target sequence.
XX
KW Zinc finger protein; vascular endothelial growth factor; VEGF; ischaemia;
KW atherosclerosis; tumour; arthritis; bone injury; wound; ulcer; surgery;
KW angiogenesis; pregnancy; embryogenesis; ds; human.
XX
OS Homo sapiens.
XX
PN US2003021776-A1.
XX
PD 30-JAN-2003.
XX
PF 06-DEC-2001; 2001US-00006069.
XX
PR 07-DEC-2000; 2000US-00733604.
PR 12-DEC-2000; 2000US-00736083.
PR 30-APR-2001; 2001US-00846033.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Rebar E, Jamieson A, Liu Q, Liu P, Wolffe A, Eisenberg SP;
PI Jarvis E;
XX
DR WPI; 2003-466074/44.
XX
PT Novel zinc finger protein that binds to a target site, useful for
PT modulating vascular endothelial growth factor gene expression, for
PT modulating angiogenesis, for wound healing and for treating ischemia.
XX
PS Disclosure; Page 43; 120pp; English.
XX
CC The invention relates to a zinc finger protein that binds to a target
CC site. The zinc finger protein is useful for modulating expression of a
CC vascular endothelial growth factor (VEGF) gene. The expression of a
CC number of splice variants of VEGF gene is modulated. A number of target
CC sites are contacted with a number of zinc finger proteins and each zinc
CC finger protein binds to a distinct target site. The zinc finger protein
CC is administered in combination with a delivery vehicle, or its nucleic
CC acid is administered into the cell, either in naked form or delivered in
CC an expression vector. The zinc finger protein or nucleic acid is useful
CC for treating a disease or injury such as atherosclerosis, ischaemia,
CC tumour, arthritis, bone injury, wounds and ulcer in a subject. The zinc
CC finger protein is also useful for modulating angiogenesis, by introducing
CC the zinc finger protein into an animal, where the animal has a genome
CC comprising a target site within a VEGF gene. The zinc finger protein is
CC also useful for screening for a modulator of expression of a VEGF gene.
CC The zinc finger protein and nucleic acid are also useful to promote
CC development of the corpus luteum and endometrium, which is useful for
CC initiating and/or maintaining pregnancy and for supporting embryogenesis.
CC The zinc finger protein and its nucleic acid are also useful in surgical
CC applications. The present sequence represents a human VEGF targetted zinc
CC finger protein ZFP target sequence
XX
SQ Sequence 9 BP; 2 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1020 TCTGCCCA 1027
||||||||
Db 8 TCTGCCCA 1

RESULT 146
ADA64108
ID ADA64108 standard; DNA; 9 BP.
XX
AC ADA64108;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #566.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX

```
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 22; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          1 AAGGTGGG 8


RESULT 147
ADA64291
ID   ADA64291 standard; DNA; 9 BP.
XX
AC   ADA64291;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #749.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          2 AGAAGGTG 9


RESULT 148
ADA64292
ID   ADA64292 standard; DNA; 9 BP.
XX
AC   ADA64292;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Zinc finger target sequence DNA #750.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          2 AGAAGGTG 9


RESULT 149
ADA64107
ID   ADA64107 standard; DNA; 9 BP.
XX
AC   ADA64107;
XX
DT   20-NOV-2003  (first entry)
```

```
XX
DE   Zinc finger target sequence DNA #565.
XX
KW   ds; target sequence; zinc finger protein;
KW   multi-finger zinc finger protein; improved affinity;
KW   improved specificity; enhanced biological activity.
XX
OS   Synthetic.
XX
PN   US2003068675-A1.
XX
PD   10-APR-2003.
XX
PF   20-NOV-2001; 2001US-00990186.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-567233/53.
XX
PT   Designing zinc finger protein that has three zinc fingers from N-terminus
PT   and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT   site, by selecting zinc fingers that bind their respective subsites.
XX
PS   Disclosure; Page 22; 34pp; English.
XX
CC   The invention relates to a method of designing a zinc finger protein. The
CC   method is useful for designing a zinc finger protein. The method provides
CC   multi-finger zinc finger proteins with improved affinity and specificity
CC   for their target sequences, as well as enhanced biological activity. The
CC   present sequence represents a zinc finger protein DNA target sequence.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          1 AAGGTGGG 8


RESULT 150
ADM22799
ID   ADM22799 standard; DNA; 9 BP.
XX
AC   ADM22799;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Synthetic zinc finger protein target DNA #565.
XX
KW   zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS   Unidentified.
XX
PN   US2003104526-A1.
XX
PD   05-JUN-2003.
XX
PF   20-NOV-2001; 2001US-00989994.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-843091/78.
XX
PT   New zinc finger protein used for recognizing triplet target subsites
PT   having nucleotide G in 5'-most position of subsite, that has been
PT   optimized with respect to location of subsite within target site.
XX
PS   Example 6; SEQ ID NO 2078; 48pp; English.
XX
CC   The invention describes a new zinc finger protein that binds to a target
CC   site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC   ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC   comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC   (S3) target subsites. The zinc finger proteins can be used for
CC   recognising triplet target subsites having the nucleotide G in the 5'-
CC   most position of the subsite, that has been optimised with respect to the
CC   location of the subsite within the target site. This sequence represents
CC   the target polynucleotide to which the zinc finger protein sp-1 consensus
CC   sequence binds.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db          1 AAGGTGGG 8


RESULT 151
ADM22984
ID   ADM22984 standard; DNA; 9 BP.
XX
AC   ADM22984;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Synthetic zinc finger protein target DNA #750.
XX
KW   zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS   Unidentified.
XX
PN   US2003104526-A1.
XX
PD   05-JUN-2003.
XX
PF   20-NOV-2001; 2001US-00989994.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-843091/78.
XX
PT   New zinc finger protein used for recognizing triplet target subsites
```

```
PT   having nucleotide G in 5'-most position of subsite, that has been
PT   optimized with respect to location of subsite within target site.
XX
PS   Example 6; SEQ ID NO 2263; 48pp; English.
XX
CC   The invention describes a new zinc finger protein that binds to a target
CC   site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC   ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC   comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC   (S3) target subsites. The zinc finger proteins can be used for
CC   recognising triplet target subsites having the nucleotide G in the 5'-
CC   most position of the subsite, that has been optimised with respect to the
CC   location of the subsite within the target site. This sequence represents
CC   the target polynucleotide to which the zinc finger protein sp-1 consensus
CC   sequence binds.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 152
ADM22983
ID   ADM22983 standard; DNA; 9 BP.
XX
AC   ADM22983;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Synthetic zinc finger protein target DNA #749.
XX
KW   zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS   Unidentified.
XX
PN   US2003104526-A1.
XX
PD   05-JUN-2003.
XX
PF   20-NOV-2001; 2001US-00989994.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-843091/78.
XX
PT   New zinc finger protein used for recognizing triplet target subsites
PT   having nucleotide G in 5'-most position of subsite, that has been
PT   optimized with respect to location of subsite within target site.
XX
PS   Example 6; SEQ ID NO 2262; 48pp; English.
XX
CC   The invention describes a new zinc finger protein that binds to a target
CC   site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC   ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC   comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC   (S3) target subsites. The zinc finger proteins can be used for
CC   recognising triplet target subsites having the nucleotide G in the 5'-
CC   most position of the subsite, that has been optimised with respect to the
CC   location of the subsite within the target site. This sequence represents
CC   the target polynucleotide to which the zinc finger protein sp-1 consensus
CC   sequence binds.
XX
SQ   Sequence 9 BP; 3 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 153
ADM22800
ID   ADM22800 standard; DNA; 9 BP.
XX
AC   ADM22800;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Synthetic zinc finger protein target DNA #566.
XX
KW   zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS   Unidentified.
XX
PN   US2003104526-A1.
XX
PD   05-JUN-2003.
XX
PF   20-NOV-2001; 2001US-00989994.
XX
PR   24-MAR-1999;   99US-0126238P.
PR   24-MAR-1999;   99US-0126239P.
PR   30-JUL-1999;   99US-0146595P.
PR   30-JUL-1999;   99US-0146615P.
PR   23-MAR-2000; 2000US-00535008.
PR   20-NOV-2000; 2000US-00716637.
XX
PA   (LIUQ/) LIU Q.
XX
PI   Liu Q;
XX
DR   WPI; 2003-843091/78.
XX
PT   New zinc finger protein used for recognizing triplet target subsites
PT   having nucleotide G in 5'-most position of subsite, that has been
PT   optimized with respect to location of subsite within target site.
XX
PS   Example 6; SEQ ID NO 2079; 48pp; English.
XX
CC   The invention describes a new zinc finger protein that binds to a target
CC   site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC   ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC   comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC   (S3) target subsites. The zinc finger proteins can be used for
CC   recognising triplet target subsites having the nucleotide G in the 5'-
CC   most position of the subsite, that has been optimised with respect to the
CC   location of the subsite within the target site. This sequence represents
CC   the target polynucleotide to which the zinc finger protein sp-1 consensus
CC   sequence binds.
XX
SQ   Sequence 9 BP; 2 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
              ||||||||
```

```
Db          1 AAGGTGGG 8


RESULT 154
AAZ79378
ID   AAZ79378 standard; DNA; 10 BP.
XX
AC   AAZ79378;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1806.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 116; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
                ||||||||
Db          2 CTTCTGCC 9


RESULT 155
AAZ77868/c
ID   AAZ77868 standard; DNA; 10 BP.
XX
AC   AAZ77868;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:296.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
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PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 72; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
                      ||||||||
Db             9 AGAAGGTG 2


RESULT 156
AAZ78273
ID   AAZ78273 standard; DNA; 10 BP.
XX
AC   AAZ78273;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:701.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 85; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
```

CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1018 CTTCTGCC 1025
||||||||
Db 2 CTTCTGCC 9

RESULT 157
AAZ78942/c
ID AAZ78942 standard; DNA; 10 BP.
XX
AC AAZ78942;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1370.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 104; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1018 CTTCTGCC 1025
              ||||||||
Db          8 CTTCTGCC 1
```

RESULT 158
AAZ77770/c
ID AAZ77770 standard; DNA; 10 BP.
XX
AC AAZ77770;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:198.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.
PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 69; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

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  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          8 TTCTGCCC 1
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RESULT 159
AAZ77870/c
ID AAZ77870 standard; DNA; 10 BP.
XX
AC AAZ77870;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:298.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.

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PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 72; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1030 AAGGTGGG 1037
             ||||||||
Db          10 AAGGTGGG 3


RESULT 160
AAZ79364/c
ID   AAZ79364 standard; DNA; 10 BP.
XX
AC   AAZ79364;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1792.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 116; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
```

```
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
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CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 1 A; 3 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
              ||||||||
Db          8 CAAGAAGG 1


RESULT 161
AAZ79551
ID   AAZ79551 standard; DNA; 10 BP.
XX
AC   AAZ79551;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell SAGE tag, SEQ ID NO:1979.
XX
KW   SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW   APC; monocyte-derived dendritic cell; differential gene expression;
KW   immunostimulatory cofactor; costimulatory factor; CTL;
KW   cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965924-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013800.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106077/09.
XX
PT   Isolated polynucleotides differentially expressed in antigen-presenting
PT   cells, useful in gene vaccines against cancer.
XX
PS   Claim 1; Page 121; 130pp; English.
XX
CC   Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts encoding
CC   immunostimulatory cofactor proteins which are preferentially or
CC   differentially expressed in monocyte-derived dendritic cells compared
CC   with monocytes. Some of the transcripts correspond to known genes or ESTs
CC   (expressed sequence tags) which were previously unknown to be
CC   preferentially or differentially expressed in dendritic cells, while
CC   other transcripts correspond to novel genes. Antigen-presenting cell
CC   (APC)-associated costimulatory factors play an important role in the
CC   activation of the cytotoxic immune response, particularly against tumour
CC   cells. Tumour antigen presentation via the MHC (major histocompatibility
CC   complex) and subsequent recognition by T-cell receptors is alone
CC   insufficient to activate a robust cytotoxic immune response that can lyse
CC   the tumour cells, immunostimulatory cofactors also being required for
CC   efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC   sequences identified using the SAGE tags have several potential uses.
CC   They may be used in vaccines to induce an immune response, particularly
CC   against a tumour antigen; to modulate the genotype of an APC; to screen
CC   for agents that modulate expression of differentially expressed genes in
CC   an APC; and as hybridisation probes/amplification primers for the
CC   diagnosis, prognosis and monitoring of diseases related to abnormal
CC   expression of these genes. Detection of the dendritic cell differentially
CC   expressed genes, or of their encoded proteins, can be used to identify
CC   cells as belonging to the monocyte lineage. Cells containing these genes
CC   can be used in active immunotherapy (or to stimulate production of a
CC   population of antigen-specific effector cells) and vectors containing
CC   them are used in gene therapy. Co-administration of tumour antigens and
CC   APC-associated costimulatory factors ensures adequate antigen
CC   presentation to endogenous APCs and upregulates the APCs for the
CC   presentation of co-stimulatory signals, migration to T cell-rich sites,
CC   secretion of T cell growth factors and secretion of chemokines for
CC   recruitment of immune effector cells
XX
SQ   Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db          2 GAAGGTGG 9


RESULT 162
AAZ83134/c
ID   AAZ83134 standard; DNA; 10 BP.
XX
AC   AAZ83134;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2368.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 123; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db         10 CTTCTGCC 3


RESULT 163
AAZ81919/c
ID   AAZ81919 standard; DNA; 10 BP.
XX
AC   AAZ81919;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1153.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 89; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
```

```
SQ   Sequence 10 BP; 1 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGAA 1031
                ||||||||
Db          8 CCCAAGAA 1


RESULT 164
AAZ84193
ID   AAZ84193 standard; DNA; 10 BP.
XX
AC   AAZ84193;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #3427.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 150; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
                ||||||||
Db          3 AAGGTGGG 10


RESULT 165
AAZ82122
ID   AAZ82122 standard; DNA; 10 BP.
XX
AC   AAZ82122;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #1356.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 95; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
```

CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1018 CTTCTGCC 1025
||||||||
Db 3 CTTCTGCC 10

RESULT 166
AAZ83647/c
ID AAZ83647 standard; DNA; 10 BP.
XX
AC AAZ83647;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2881.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 136; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTG 1035
||||||||
Db 9 AGAAGGTG 2

RESULT 167
AAZ83418/c
ID AAZ83418 standard; DNA; 10 BP.
XX
AC AAZ83418;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2652.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 130; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based

```
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          9 TTCTGCCC 2


RESULT 168
AAZ82784
ID   AAZ82784 standard; DNA; 10 BP.
XX
AC   AAZ82784;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2018.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 113; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db          3 GAAGGTGG 10


RESULT 169
AAZ85883/c
ID   AAZ85883 standard; DNA; 10 BP.
XX
AC   AAZ85883;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5117.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 194; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
```

```
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db         10 GAAGGTGG 3


RESULT 170
AAZ86535
ID   AAZ86535 standard; DNA; 10 BP.
XX
AC   AAZ86535;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell downregulated transcript tag #5769.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 210; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db          2 GAAGGTGG 9


RESULT 171
AAZ81064
ID   AAZ81064 standard; DNA; 10 BP.
XX
AC   AAZ81064;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #298.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 66; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
```

CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1029 GAAGGTGG 1036
              ||||||||
Db          2 GAAGGTGG 9
```

RESULT 172
AAZ83296
ID AAZ83296 standard; DNA; 10 BP.
XX
AC AAZ83296;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #2530.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 127; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effecter
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1018 CTTCTGCC 1025
              ||||||||
Db          2 CTTCTGCC 9
```

RESULT 173
AAZ84897
ID AAZ84897 standard; DNA; 10 BP.
XX
AC AAZ84897;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #4131.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 169; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour

```
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          3 AGAAGGTG 10


RESULT 174
AAZ81128/c
ID   AAZ81128 standard; DNA; 10 BP.
XX
AC   AAZ81128;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #362.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 67; 219pp; English.
XX
```

```
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          8 TTCTGCCC 1


RESULT 175
AAZ83682
ID   AAZ83682 standard; DNA; 10 BP.
XX
AC   AAZ83682;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #2916.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
```

```
PS   Claim 1; Page 137; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db          1 GAAGGTGG 8


RESULT 176
AAZ83851
ID   AAZ83851 standard; DNA; 10 BP.
XX
AC   AAZ83851;
XX
DT   07-APR-2000  (first entry)
XX
DE   Metastatic breast tumour cell upregulated transcript tag #3085.
XX
KW   Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW   non-metastatic breast tumour tissue; gene therapy; anticancer;
KW   antimetastatic; vaccine; diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9965928-A2.
XX
PD   23-DEC-1999.
XX
PF   18-JUN-1999;   99WO-US013647.
XX
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0090039P.
PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106079/09.
XX
PT   Isolated polynucleotides differentially expressed between metastatic and
PT   non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT   treatment of cancer.
XX
PS   Claim 1; Page 141; 219pp; English.
XX
CC   AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC   that are preferentially transcribed in the metastatic breast tumour
CC   tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC   to AAZ86677 represent tags corresponding to distinct transcripts that are
CC   preferentially transcribed in the primary or non-metastatic breast tumour
CC   tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC   transcripts can be used for diagnosis, prognosis, monitoring and
CC   treatment of breast cancer, particularly where metastatic. Diagnosis is
CC   by standard immunoassays or hybridisation/amplification reactions.
CC   Compounds that modulate expression of the transcripts are potentially
CC   useful for treatment of (metastatic) breast cancer, while promoters from
CC   the transcripts are used to direct expression, in selected cell types, of
CC   e.g. therapeutic genes (also ribozymes or antisense sequences),
CC   particularly an antigen-encoding sequence for use in gene or cell-based
CC   vaccines. Polypeptides encoded by the transcripts are also useful in
CC   vaccines; for diagnosing breast cancer and for raising specific
CC   antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC   agents. Host cells that produce the polypeptides can be used to expand
CC   and isolate populations of educated, antigen-specific immune effecter
CC   cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC   immunotherapy
XX
SQ   Sequence 10 BP; 0 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          1 TTCTGCCC 8


RESULT 177
AAZ79914/c
ID   AAZ79914 standard; DNA; 10 BP.
XX
AC   AAZ79914;
XX
DT   10-APR-2000  (first entry)
XX
DE   Human dendritic cell preferentially expressed SAGE tag, SEQ ID NO:205.
XX
KW   SAGE tag; serial analysis of gene expression; diagnosis;
KW   differential gene expression; characterisation; targetted expression;
KW   tumour; cancer; immunotherapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9966303-A2.
XX
PD   23-DEC-1999.
XX
PF   17-JUN-1999;   99WO-US013820.
XX
PR   19-JUN-1998;   98US-0089833P.
PR   19-JUN-1998;   98US-0089844P.
PR   19-JUN-1998;   98US-0089853P.
PR   19-JUN-1998;   98US-0089878P.
PR   19-JUN-1998;   98US-0089991P.
PR   19-JUN-1998;   98US-0089992P.
PR   19-JUN-1998;   98US-0089993P.
PR   19-JUN-1998;   98US-0089994P.
PR   19-JUN-1998;   98US-0089997P.
PR   19-JUN-1998;   98US-0089999P.
PR   19-JUN-1998;   98US-0090000P.
PR   19-JUN-1998;   98US-0090035P.
PR   19-JUN-1998;   98US-0090036P.
PR   19-JUN-1998;   98US-0090039P.
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PR   19-JUN-1998;   98US-0090040P.
PR   19-JUN-1998;   98US-0090041P.
PR   19-JUN-1998;   98US-0090042P.
PR   19-JUN-1998;   98US-0090043P.
PR   19-JUN-1998;   98US-0090044P.
PR   19-JUN-1998;   98US-0090045P.
PR   19-JUN-1998;   98US-0090047P.
PR   19-JUN-1998;   98US-0090048P.
PR   19-JUN-1998;   98US-0090072P.
PR   19-JUN-1998;   98US-0090076P.
PR   19-JUN-1998;   98US-0090077P.
PR   19-JUN-1998;   98US-0090078P.
PR   19-JUN-1998;   98US-0090079P.
PR   19-JUN-1998;   98US-0090080P.
PR   08-DEC-1998;   98US-0111715P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (ROBE/) ROBERTS B L.
PA   (SHAN/) SHANKARA S.
XX
PI   Roberts BL,  Shankara S;
XX
DR   WPI; 2000-106132/09.
XX
PT   New polynucleotide useful in cancer immunotherapy.
XX
PS   Claim 1; Page 63; 97pp; English.
XX
CC   Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene
CC   expression) tags used to identify mRNA transcripts which are
CC   differentially expressed in a variety of normal or malignant cell types.
CC   Some of the transcripts correspond to known genes or ESTs (expressed
CC   sequence tags) which were previously unknown to be preferentially or
CC   differentially expressed in that particular cell type, while other
CC   transcripts correspond to novel genes. The invention also provides a
CC   nucleotide comprising a promoter sequence derived from one of the
CC   differentially expressed genes, which may optionally be operably linked
CC   to a foreign nucleotide sequence, and gene delivery vehicles and host
CC   cells comprising the polynucleotides of the invention. A nucleotide
CC   comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures
CC   to characterise a cell of a specific tissue type and to determine whether
CC   it is normal or malignant. They may be used to screen for agents that
CC   modulate expression of differentially expressed genes compound. The
CC   promoter/foreign gene construct of the invention may be used for
CC   targetted expression of the foreign gene in a particular cell type. For
CC   example, a promoter derived from a gene preferentially expressed in
CC   dendritic cells (antigen-presenting cells, or APCs), may be operably
CC   linked to a sequence encoding an immunostimulatory molecule and a
CC   sequence encoding an antigen. Such a construct could be transduced into
CC   APCs and would be useful for inducing an immune response by educating
CC   immune effector cells in vivo, or in cancer immunotherapy
XX
SQ   Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db         10 AAGGTGGG 3


RESULT 178
AAH64317
ID   AAH64317 standard; cDNA; 10 BP.
XX
AC   AAH64317;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1157.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 13; Page 65; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          3 AGAAGGTG 10


RESULT 179
AAH63292/c
ID   AAH63292 standard; cDNA; 10 BP.
XX
AC   AAH63292;
XX
DT   20-SEP-2001  (first entry)
XX
DE   Human colon epithelium specific transcriptome sequence SEQ ID NO: 132.
XX
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;
KW   cancer diagnosis; cell specific gene expression; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138577-A2.
XX
PD   31-MAY-2001.
XX
PF   21-NOV-2000; 2000WO-US031922.
XX
PR   24-NOV-1999;   99US-00448480.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu VE,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2001-367706/38.
```

```
XX
PT   New isolated polynucleotides, useful for identifying specific cell type,
PT   such as cancer cell, comprises transcriptomes expressed in particular
PT   cell types.
XX
PS   Claim 11; Page 42; 94pp; English.
XX
CC   The present invention describes a method of identifying the type of cell
CC   in a sample, involving determining which of the sequences AAH63161-
CC   AAH64724 is expressed by the cell. The transcriptomes described in the
CC   invention are cell-type specific, cancer specific or ubiquitously
CC   expressed in humans. They can also be used to screen for drugs, reduce
CC   cancer specific gene expression, standardise expression and restore the
CC   function of a diseased cell or tissue. The present sequence is one of the
CC   transcriptomes described in the exemplification of the invention
XX
SQ   Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
             ||||||||
Db          8 CAAGAAGG 1


RESULT 180
AAF69638
ID   AAF69638 standard; DNA; 10 BP.
XX
AC   AAF69638;
XX
DT   18-APR-2001  (first entry)
XX
DE   Human IL4Ralpha gene probe #278.
XX
KW   Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW   allergic disease; probe; ss.
XX
OS   Homo sapiens.
XX
PN   WO200104270-A1.
XX
PD   18-JAN-2001.
XX
PF   13-JUL-2000; 2000WO-US019094.
XX
PR   13-JUL-1999;   99US-0143435P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Chew A,  Denton RR,  Duda A,  Nandabalan K,  Stephens JC;
PI   Windemuth AK;
XX
DR   WPI; 2001-103078/11.
XX
PT   New isolated polynucleotide useful for the identification of therapeutics
PT   in allergic diseases is new.
XX
PS   Disclosure; Page 46; 188pp; English.
XX
CC   The present invention relates to polymorphisms of the human interleukin 4
CC   receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference
CC   sequence). Polynucleotides comprising polymorphic gene variants are
CC   useful for therapeutic purposes. For example, where a patient may benefit
CC   from expression of a particular IL4Ralpha protein isoform, an expression
CC   vector encoding the isoform may be administered to the patient. It may
CC   desirable to decrease or block expression of a particular IL4Ralpha
CC   isogene, which may be done by turning off by transforming a targeted
CC   organ, tissue or cell population with an expression vector that expresses
CC   high levels of untranslatable mRNA for the isogene. Specific therapeutics
CC   identified by these methods may be useful for allergic diseases. The
CC   present sequence is a probe for human IL4R-alpha
XX
SQ   Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
             ||||||||
Db          3 GAAGGTGG 10


RESULT 181
AAF35751
ID   AAF35751 standard; DNA; 10 BP.
XX
AC   AAF35751;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2490.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 88; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
```

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 4 A; 0 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1027 AAGAAGGT 1034
||||||||
Db 1 AAGAAGGT 8

RESULT 182
AAF39472/c
ID AAF39472 standard; DNA; 10 BP.
XX
AC AAF39472;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6211.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 221; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1025 CCAAGAAG 1032
||||||||
Db 9 CCAAGAAG 2

RESULT 183
AAF39102/c
ID AAF39102 standard; DNA; 10 BP.
XX
AC AAF39102;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5841.
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX
DR WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 208; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a

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CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAA 1028
              ||||||||
Db         10 CTGCCCAA 3


RESULT 184
AAF41579/c
ID   AAF41579 standard; DNA; 10 BP.
XX
AC   AAF41579;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8318.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 297; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAG 1032
              ||||||||
Db          8 CCAAGAAG 1


RESULT 185
AAF43940
ID   AAF43940 standard; DNA; 10 BP.
XX
AC   AAF43940;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12079.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 381; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
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CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 0 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
              ||||||||
Db          2 TTCTGCCC 9


RESULT 186
AAF34735
ID   AAF34735 standard; DNA; 10 BP.
XX
AC   AAF34735;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1474.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 52; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 5 A; 1 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
              ||||||||
Db          2 CAAGAAGG 9


RESULT 187
AAF34229
ID   AAF34229 standard; DNA; 10 BP.
XX
AC   AAF34229;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:968.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 34; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
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```
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          3 AGAAGGTG 10


RESULT 188
AAF37328
ID   AAF37328 standard; DNA; 10 BP.
XX
AC   AAF37328;
XX
DT   23-MAR-2001  (first entry)
XX
DE   Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4067.
XX
KW   Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW   nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW   serial analysis of gene expression; antifungal; tag; identification;
KW   linker; PCR primer; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200077214-A2.
XX
PD   21-DEC-2000.
XX
PF   14-JUN-2000; 2000WO-US016223.
XX
PR   16-JUN-1999;   99US-00335032.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Velculescu V,  Vogelstein B,  Kinzler K;
XX
DR   WPI; 2001-061874/07.
XX
PT   Yeast gene coding sequences comprising NORF genes with serial analysis of
PT   gene expression (SAGE) tags, useful for studying, monitoring and
PT   affecting phases of the cell cycle.
XX
PS   Example; Page 145; 419pp; English.
XX
CC   The present invention describes an isolated DNA molecule comprising a
CC   coding sequence of a yeast gene selected from a group of 745 NORF (not
CC   previously assigned open reading frame; or nonannotated ORF) genes
CC   comprising a SAGE (serial analysis of gene expression) tag. Also
CC   described are: (1) a method (M1) of using NORF genes to affect the cell
CC   cycle comprising administering a NORF gene whose expression varies by at
CC   least 10% between any two phases of the cell cycle selected from log
CC   phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC   antifungal drugs comprising: (a) contacting a test substance with a yeast
CC   cell; and (b) monitoring expression of a NORF gene whose expression
CC   varies as in M1, where a test substance which modifies the expression of
CC   the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC   identifying human genes which are involved in cell cycle progression
CC   comprising contacting human DNA with a probe which comprises at least 10
CC   contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC   and (4) a method (M4) for identifying a candidate drug as a member of a
CC   class of drugs having a characteristic effect on gene expression in a
CC   yeast cell comprising contacting a yeast cell with a candidate drug and
CC   monitoring expression in the yeast cell of at least 1 NORF gene whose
CC   expression is affected by the class of drugs. The NORF genes may be used
CC   to study, monitor and affect phases of the cell cycle, the differentially
CC   expressed genes may be used as markers of phases of the cell cycle. The
CC   methods may be used to identify candidate drugs which affect the cell
CC   cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC   represent SAGE tags used in the exemplification of the present invention.
CC   AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC   method, in the exemplification of the present invention
XX
SQ   Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
              ||||||||
Db          1 CAAGAAGG 8


RESULT 189
ABK24258
ID   ABK24258 standard; DNA; 10 BP.
XX
AC   ABK24258;
XX
DT   09-APR-2002  (first entry)
XX
DE   Retinaldehyde-binding protein 1 ASO primer extension primer #31.
XX
KW   Human; retinaldehyde-binding protein 1; ss; RLBP1; haplotype; primer;
KW   genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR;
KW   chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.
XX
OS   Homo sapiens.
XX
PN   WO200192278-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US017252.
XX
PR   26-MAY-2000; 2000US-0207618P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Choi JY,  Kazemi A,  Koshy B;
XX
DR   WPI; 2002-122053/16.
XX
PT   New genetic variants having polymorphisms in the retinaldehyde-binding
PT   protein 1 gene, useful for studying the function of and for expressing
PT   RLBP1 protein for use in screening drugs for treating diseases related to
PT   RLBP1 activity.
XX
PS   Claim 18; Page 14; 107pp; English.
```

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XX
CC   The invention relates to an isolated polynucleotide, which comprises
CC   genes and haplotypes of the retinaldehyde-binding protein 1 (RLBP1) gene.
CC   The polynucleotide comprises polymorphic sites in the RLBP1 gene, which
CC   are referred to as PS1-24 to designate the order in which they are
CC   located in the gene. Also included are methods for haplotyping or
CC   genotyping the RLBP1 gene of an individual, a method for predicting a
CC   haplotype pair for the RLBP1 gene of an individual, a method for
CC   identifying an association between a trait and at least one haplotype or
CC   haplotype pair of the RLBP1 gene, a composition comprising at least one
CC   genotyping oligonucleotide for detecting a polymorphism in the RLBP1 gene
CC   at a PS consisting of PS1-PS24, a kit for genotyping the RLBP1 gene of an
CC   individual comprising a set of oligonucleotides designed to genotype each
CC   of PS1-PS24 recombinant non-human organisms transformed or transfected
CC   with the isolated polynucleotide, where the organism expresses a RLBP1
CC   protein encoded by the first nucleotide sequence or expresses an RLBP1
CC   protein encoded by the polymorphic variant sequence, an isolated
CC   polypeptide comprising an amino acid sequence that is a polymorphic
CC   variant of a reference sequence for the RLBP1 protein or its fragment, an
CC   anti-RLBP1 antibody, a method for screening for drugs targeting the
CC   isolated polypeptide, and a computer system for storing and analysing
CC   polymorphism data for the RLBP1 oncogene gene. The polynucleotide
CC   comprising polymorphisms in the RLBP1 gene is useful in studying the
CC   expression and function of RLBP1, and in expressing RLBP1 protein for use
CC   in screening candidate drugs to treat diseases related to RLBP1 activity
CC   (e.g autosomal recessive retinitis pigmentosa (arRP). The methods and
CC   haplotypes are useful in improving the efficiency and output of several
CC   steps in the drug discovery and development process, including target
CC   validation, identifying lead compounds, and early phase clinical trials.
CC   These are also useful for designing clinical trials of candidate drugs
CC   for treating a specific condition or disease, as well as for screening
CC   compounds targeting RLBP1 to treat a specific condition or disease
CC   predicted to be associated with RLBP1 activity. The kit and method are
CC   useful for determining whether an individual has one of the haplotypes or
CC   haplotype pairs cited above. The transgenic animals are useful for
CC   studying expression of the RLBP1 isogenes in vivo, for in vivo screening
CC   and testing of drugs targeted against RLBP1 protein, and for testing the
CC   efficacy of therapeutic agents and compounds for retinal diseases in a
CC   biological system. The gene for RLBP1 is located on chromosome 15q26. The
CC   present sequence is an allele specific oligonucleotide (ASO) PCR primer
CC   for amplifying a nucleic acid containing a polymorphic RLBP sequence,
CC   using the primer extension method
XX
SQ   Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGA 1030
             ||||||||
Db          1 GCCCAAGA 8


RESULT 190
ABK23697
ID   ABK23697 standard; DNA; 10 BP.
XX
AC   ABK23697;
XX
DT   09-APR-2002  (first entry)
XX
DE   Transcript tag DNA sequence #286 induced or suppressed by N-myc.
XX
KW   Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;
KW   spread; myc target; myc tag; SAGE; serial analysis of gene expression;
KW   myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200185941-A2.
XX
PD   15-NOV-2001.
XX
PF   11-MAY-2001; 2001WO-NL000361.
XX
PR   11-MAY-2000; 2000EP-00201698.
PR   29-JUN-2000; 2000EP-00202284.
XX
PA   (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.
XX
PI   Versteeg R,  Caron HN;
XX
DR   WPI; 2002-066603/09.
XX
PT   A new nucleic acid library of myc-dependent downstream genes capable of
PT   supporting a neoplastic characteristic of cancer is useful to find new
PT   therapies and diagnoses for cancer.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   The present invention relates to a nucleic acid library comprising myc-
CC   dependent downstream genes or their functional fragments essentially
CC   capable of supporting a neoplastic character of cancer such as growth,
CC   invasion or spread. These myc target or tag sequences are identified by
CC   SAGE (serial analysis of gene expression). The library is useful to find
CC   new diagnoses and treatments for cancer. The invention is also useful to
CC   enhance production of recombinant proteins in a production system with
CC   high expression of endogenous or transfected myc oncogenes. ABK23412-
CC   ABK23828 represent transcript tag DNA sequences that are activated or
CC   repressed by N-myc in human neuroblastoma
XX
SQ   Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
             ||||||||
Db          2 CTTCTGCC 9


RESULT 191
AAS16818/c
ID   AAS16818 standard; DNA; 10 BP.
XX
AC   AAS16818;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human apolipoprotein C1 (APOC1) gene PCR primer #4.
XX
KW   Human; apolipoprotein C1; APOC1; single nucleotide polymorphism;
KW   haplotyping; haplotype pair; hypercholesterolaemia; nootropic; SDAT; ss;
KW   senile dementia of Alzheimer's type; neuroprotective; antilipaemic;
KW   PCR primer.
XX
OS   Homo sapiens.
XX
PN   WO200177129-A2.
XX
PD   18-OCT-2001.
XX
PF   10-APR-2001; 2001WO-US011808.
XX
PR   11-APR-2000; 2000US-0196545P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
XX
PI   Bentivegna SC,  Chew A,  Choi JY,  Koshy B,  Stephens JC;
XX
DR   WPI; 2002-041286/05.
XX
PT   New haplotypes of the human apolipoprotein C1 gene, useful to detect and
PT   find treatment for disease associated with its activity such as
```

PT hypercholestrolemia and Alzheimer's disease.
XX
PS Claim 18; Page 13; 51pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the human
CC apolipoprotein C1 (APOC1) gene. Haplotyping the APOC1 gene of an
CC individual, comprises determining if the individual has one of the APOC1
CC haplotypes or haplotype pairs fully defined in the specification.
CC Genotyping the APOC1 gene of an individual, comprises determining the
CC identity of the nucleotide pair at one or more polymorphic sites and
CC predicting a haplotype pair for the APOC1 gene of an individual by
CC enumerating all possible haplotype pairs which are consistent with the
CC genotype, comparing the possible haplotype pairs to the data detailed in
CC the specification and assigning a haplotype pair to the individual that
CC is consistent with the data. Identifying an association between a trait
CC and a haplotype or haplotype pair of the APOC1 gene, comprises comparing
CC the frequency of the haplotype/haplotype pair in a population exhibiting
CC the trait with that of a reference population, where the
CC haplotype/haplotype pair is one described in the specification and a
CC higher frequency in the trait population indicates the trait is
CC associated with the haplotype. The sequences and methods of the invention
CC are used to diagnose and develop treatment for disease associated with
CC APOC1 activity, such as hypercholesterolaemia and senile dementia of
CC Alzheimer's type (SDAT). This sequence represents a PCR primer used for
CC detecting human APOC1 DNA polymorphisms
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1029 GAAGGTGG 1036
||||||||
Db 9 GAAGGTGG 2

RESULT 192
ADC09948/c
ID ADC09948 standard; DNA; 10 BP.
XX
AC ADC09948;
XX
DT 18-DEC-2003 (first entry)
XX
DE Optical nucleic acid sensor molecule-related oligo, SEQ ID 360.
XX
KW Nucleic acid sensor molecule; ligase; cis-hammerhead; protein kinase; ds.
XX
OS Synthetic.
XX
PN WO2003014375-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025319.
XX
PR 09-AUG-2001; 2001US-0311378P.
PR 21-AUG-2001; 2001US-0313932P.
PR 13-SEP-2001; 2001US-0952680.
PR 13-NOV-2001; 2001US-0338186P.
PR 18-JAN-2002; 2002US-0349959P.
PR 13-MAR-2002; 2002US-0364486P.
PR 25-MAR-2002; 2002US-0367991P.
PR 04-APR-2002; 2002US-0369887P.
PR 01-MAY-2002; 2002US-0376744P.
PR 31-MAY-2002; 2002US-0385097P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N, Kurz M, Keefe T, Wilson C;
PI Grate D, Marshall KA, Mccauley T, Kurz J;
XX
DR WPI; 2003-300534/29.
XX
PT Nucleic acid sensor molecule, for identifying/detecting protein kinase in
PT a sample, comprises a target modulation domain which recognizes a target
PT molecule, a linker domain, a catalytic domain, and an optical signal
PT generator.
XX
PS Example 39; SEQ ID NO 360; 423pp; English.
XX
CC The present invention relates to nucleic acid sensor molecules (I), which
CC comprise a target modulation domain that recognizes a target molecule
CC (TM), a linker domain, a catalytic domain, and an optical signal
CC generating unit. The catalytic domain comprises a ligase or cis-
CC hammerhead. (I) are useful for identifying or detecting TM in a sample,
CC preferably a protein kinase in a sample. Target molecules include
CC proteins, post-translationally modified forms of proteins, peptides,
CC nucleic acids, oligosaccharides, nucleotides, metabolites, drugs, toxins,
CC biohazards, ions, carbohydrates, polysaccharides, hormones, receptors,
CC antigens, antibodies, viruses, metabolites, co-factors, drugs, dyes,
CC nutrients, growth factors, cCMP, cAMP or cGMP, protein kinase,
CC phosphorylated protein kinase, extracellular signal regulated kinase
CC (ERK), a component or product of mitogen activated protein (MAP) kinase
CC pathway, a MAP kinase pathway associated protein, an extracellular
CC component of MAP kinase pathway, a component of ERK1/2 MAP, JNK MAP or
CC P38 MAP kinase pathway, an endogenous form of MAP kinase (MEK), MAP
CC kinase kinase, or MAP kinase (MEKKK), or RAF kinase, Ras protein,
CC phosphatase, GTP binding protein, G-protein coupled receptor (GPCR),
CC cytokine, growth factor, cellular metabolite, small molecule or lysozyme.
CC (I) are also useful for identifying a modulator of protein kinase
CC activity. The present sequence was used to illustrate the invention.
XX
SQ Sequence 10 BP; 0 A; 1 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1024 CCCAAGAA 1031
||||||||
Db 9 CCCAAGAA 2

RESULT 193
ADI13743
ID ADI13743 standard; DNA; 10 BP.
XX
AC ADI13743;
XX
DT 22-APR-2004 (first entry)
XX
DE Cytoplasmic tumour endothelial marker standard tag SEQ ID NO:118.
XX
KW tumour endothelial marker; TEM; endothelial cell regulation;
KW neoangiogenesis inhibition; neoangiogenesis screening;
KW neoangiogenesis promotion; neoangiogenesis; tumour; wound healing;
KW cytostatic; vulnerary; human; standard tag; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004005883-A2.
XX
PD 15-JAN-2004.
XX
PF 02-JUL-2003; 2003WO-US016250.
XX
PR 02-JUL-2002; 2002US-0393023P.
PR 01-APR-2003; 2003US-0458964P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI St Croix B, Kinzler KW, Vogelstein B;
XX

```
DR   WPI; 2004-142995/14.
XX
PT   Use of tumor endothelial marker proteins for inhibiting neoangiogenesis,
PT   screening for neoangiogenesis, promoting neoangiogenesis, identifying
PT   candidate drugs for treating tumors or promoting wound healing.
XX
PS   Disclosure; SEQ ID NO 118; 113pp; English.
XX
CC   The present invention describes the use of tumour endothelial marker
CC   (TEM) proteins for identifying a ligand involved in endothelial cell
CC   regulation, inhibiting neoangiogenesis, screening for neoangiogenesis,
CC   promoting neoangiogenesis, identifying candidate drugs for treating
CC   tumours or promoting wound healing or identifying endothelial cells. Also
CC   described: (1) identification of a ligand involved in endothelial cell
CC   regulation; (2) inhibiting neoangiogenesis; (3) promoting neoangiogenesis
CC   in a patient; (4) screening for neoangiogenesis in a patient; (5)
CC   identify candidate drugs for treating tumours or promoting wound healing;
CC   and (6) identifying endothelial cells. TEM proteins have cytostatic and
CC   vulnerary activities. The TEM proteins are useful for identifying a
CC   ligand involved in endothelial cell regulation, inhibiting
CC   neoangiogenesis, screening for neoangiogenesis, promoting
CC   neoangiogenesis, identifying candidate drugs for treating tumours or
CC   promoting wound healing or identifying endothelial cells. The present
CC   sequence represents a cytoplasmic tumour endothelial marker standard tag
CC   oligonucleotide, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db          2 CTTCTGCC 9


RESULT 194
ADK13070
ID   ADK13070 standard; DNA; 10 BP.
XX
AC   ADK13070;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human glioma endothelial marker (GEM) standard tag SEQ ID NO:248.
XX
KW   glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;
KW   anticancer; antiglioma; immune response; cytostatic;
KW   multi-drug sensitive glioma; human; standard tag; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004016758-A2.
XX
PD   26-FEB-2004.
XX
PF   15-AUG-2003; 2003WO-US025614.
XX
PR   15-AUG-2002; 2002US-0403390P.
PR   01-APR-2003; 2003US-0458978P.
XX
PA   (GENZ ) GENZYME CORP.
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Madden SI,  Wang CJ,  Cook BP,  Lattera J,  Walter K;
XX
DR   WPI; 2004-247973/23.
XX
PT   Diagnosing glioma by detecting expression product of any one of 255
PT   genes, glioma endothelial markers, in brain tissue sample suspected of
PT   being neoplastic, and comparing the expression with expression in normal
PT   brain tissue sample.
XX
PS   Example 2; SEQ ID NO 248; 114pp; English.
XX
CC   The present invention describes a method (M1) for aiding in the diagnosis
CC   of glioma. (M1) involves detecting an expression product of at least one
CC   gene (I) in a first brain tissue sample (T) suspected of being
CC   neoplastic, where (I) is chosen from any one of 255 genes (glioma
CC   endothelial markers (GEMs)) as given in specification, and comparing the
CC   expression of (I) in (T) with expression of (I) in a second normal brain
CC   tissue sample (R), where increased expression of (I) in (T) relative to
CC   (R), identifies (T) as likely to be neoplastic. Also described: (1)
CC   treating (M2) glioma involves contacting cells of the glioma with an
CC   antibody that specifically binds to a extracellular epitope; (2)
CC   identifying (M3) a test compound as potential anticancer or antiglioma
CC   drug involves contacting a test compound with the cell which expresses
CC   (I), monitoring an expression product of the at least one gene and
CC   identifying test compound as a potential anticancer drug if it decreases
CC   the expression of at least one gene; (3) identifying (M4) a test compound
CC   as potential anticancer or antiglioma drug involves contacting a test
CC   compound with the cell which expresses mRNA of at least one gene
CC   identified by a tag as described above, monitoring mRNA of the gene, and
CC   identifying the test compound as a potential anticancer drug if it
CC   decreases the expression of at least one gene; and (4) inducing (M5) an
CC   immune response to glioma involves administering to a mammal, a protein
CC   or (I). (I) have cytostatic activities, and can be used to trigger immune
CC   destruction of glioma cells, and as immune response inducers. (M1) is
CC   useful for aiding in diagnosing glioma. (M2) is useful for treating multi
CC   -drug sensitive glioma in a human. (M5) is useful for inducing an immune
CC   response to a glioma in a mammal having glioma or in a mammal who has had
CC   a glioma surgically removed. The present sequence represents a human GEM
CC   standard tag oligonucleotide, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 10 BP; 0 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db          3 CTTCTGCC 10


RESULT 195
ADM57243
ID   ADM57243 standard; DNA; 10 BP.
XX
AC   ADM57243;
XX
DT   03-JUN-2004  (first entry)
XX
DE   A thaliana herbicide target related adaptor sequence #2.
XX
KW   ss; adaptor; plant; herbicide; cress.
XX
OS   Synthetic.
XX
PN   WO2004022780-A2.
XX
PD   18-MAR-2004.
XX
PF   30-JUL-2003; 2003WO-EP008393.
XX
PR   16-AUG-2002; 2002DE-01038434.
XX
PA   (META-) METANOMICS GMBH & CO KGAA.
XX
PI   Plesch G,  Blau A,  Daeschner K;
XX
DR   WPI; 2004-315575/29.
```

XX
PT Identifying herbicides and growth regulators, comprises testing compounds
PT for activity against specific nucleic acid or encoded proteins, also
PT preparation of herbicide-tolerant plants.
XX
PS Example 2; Page 70; 205pp; German.
XX
CC The present invention relates to a method for identifying substances with
CC herbicidal activity from their ability to reduce or block the expression
CC or activity of specific genes or nucleic acids or the amino acid
CC sequences encoded by them. In particular, the sequences are from
CC Arabidopsis thaliana. The method can identify herbicides with species-
CC independent activity and can be used to screen combinatorial libraries.
CC The present sequence is an adaptor sequence used in the exemplification
CC of the invention.
XX
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 40.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1021 CTGCCCAA 1028
||||||||
Db 3 CTGCCCAA 10

Search completed: December 3, 2004, 11:40:34
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:41:56 ; Search time 0.001 Seconds
(without alignments)
14.120 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cttctgcccaagaaggtggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 36 seqs, 353 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 36 summaries

Database : rnidb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	9	45.0	11	1	US-09-862-847-15	Sequence 15, Appl
c	2	9	45.0	12	1	US-09-862-844-6	Sequence 6, Appli
c	3	9	45.0	12	1	US-09-862-844-8	Sequence 8, Appli
	4	8.4	42.0	10	1	US-08-410-779B-47	Sequence 47, Appl
c	5	8.4	42.0	10	1	US-09-508-753B-225	Sequence 225, App
	6	8.4	42.0	10	1	PCT-US95-04477-47	Sequence 47, Appl
	7	8.4	42.0	11	1	US-08-401-512-15	Sequence 15, Appl
	8	8.4	42.0	11	1	US-08-481-658B-73	Sequence 73, Appl
	9	8.4	42.0	11	1	US-08-477-504A-73	Sequence 73, Appl
	10	8.4	42.0	11	1	US-08-486-756A-73	Sequence 73, Appl
	11	8.4	42.0	11	1	US-08-485-862B-73	Sequence 73, Appl
	12	8.4	42.0	11	1	US-08-787-739-73	Sequence 73, Appl
	13	8.4	42.0	11	1	US-08-487-077A-73	Sequence 73, Appl
	14	8.4	42.0	11	1	US-08-485-863A-73	Sequence 73, Appl
	15	8.4	42.0	11	1	US-08-485-049D-73	Sequence 73, Appl
	16	8.4	42.0	11	1	US-09-178-115-73	Sequence 73, Appl
	17	8.4	42.0	11	1	US-09-177-776-73	Sequence 73, Appl
	18	8.4	42.0	11	1	US-09-772-719B-73	Sequence 73, Appl
	19	8	40.0	10	1	US-08-049-283A-31	Sequence 31, Appl
	20	8	40.0	10	1	US-08-049-283A-33	Sequence 33, Appl
	21	8	40.0	10	1	US-09-508-753B-70	Sequence 70, Appl
	22	7.4	37.0	9	1	US-08-437-013-6	Sequence 6, Appli
	23	7.4	37.0	9	1	US-09-275-506A-6	Sequence 6, Appli
	24	7.4	37.0	9	1	US-09-639-576-2	Sequence 2, Appli
	25	7	35.0	8	1	US-08-593-345B-19	Sequence 19, Appl
	26	7	35.0	8	1	US-08-859-954-55	Sequence 55, Appl
	27	7	35.0	8	1	US-08-859-954-248	Sequence 248, App
	28	7	35.0	8	1	US-08-859-954-249	Sequence 249, App
	29	7	35.0	8	1	US-08-859-954-267	Sequence 267, App
	30	7	35.0	8	1	US-08-859-954-406	Sequence 406, App
	31	7	35.0	8	1	US-08-859-954-540	Sequence 540, App
	32	7	35.0	8	1	US-08-855-372B-6	Sequence 6, Appli
	33	7	35.0	8	1	US-09-498-851-6	Sequence 6, Appli
c	34	7	35.0	9	1	US-08-068-945A-36	Sequence 36, Appl
c	35	7	35.0	9	1	US-08-442-806-36	Sequence 36, Appl
	36	7	35.0	9	1	US-09-063-450-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-862-847-15/c
; Sequence 15, Application US/09862847
; Patent No. 6593111
; GENERAL INFORMATION:
; APPLICANT: Baric, Ralph S.
; APPLICANT: Boyd, Yount
; TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
; FILE REFERENCE: 5470.270
; CURRENT APPLICATION NUMBER: US/09/862,847
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/206,537
; PRIOR FILING DATE: 2000-05-21
; PRIOR APPLICATION NUMBER: US 60/285,320
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

Query Match 45.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1025 CCAAGAAGG 1033
              |||||||||
Db         10 CCAAGAAGG 2
```

RESULT 2
US-09-862-844-6/c
; Sequence 6, Application US/09862844
; Patent No. 6583986
; GENERAL INFORMATION:
; APPLICANT: Cai, Hong
; APPLICANT: Keller, Richard
; APPLICANT: Werner, James
; APPLICANT: Goodwin, Peter
; TITLE OF INVENTION: RAPID HAPLOTYPING BY SINGLE MOLECULE DETECTION
; FILE REFERENCE: S-94,652
; CURRENT APPLICATION NUMBER: US/09/862,844
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: DNA
; ORGANISM: PNA probe MLLCy5P
US-09-862-844-6

Query Match 45.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1023 GCCCAAGAA 1031
              |||||||||
Db         10 GCCCAAGAA 2
```

RESULT 3

```
US-09-862-844-8/c
; Sequence 8, Application US/09862844
; Patent No. 6583986
; GENERAL INFORMATION:
;  APPLICANT: Cai, Hong
;  APPLICANT:  Keller, Richard
;  APPLICANT:  Werner, James
;  APPLICANT:  Goodwin, Peter
;  TITLE OF INVENTION: RAPID HAPLOTYPING BY SINGLE MOLECULE DETECTION
;  FILE REFERENCE: S-94,652
;  CURRENT APPLICATION NUMBER: US/09/862,844
;  CURRENT FILING DATE:  2001-05-21
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: LNA probe MLLCy5L
US-09-862-844-8

  Query Match             45.0%;  Score 9;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.9;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAA 1031
             |||||||||
Db         10 GCCCAAGAA 2


RESULT 4
US-08-410-779B-47
; Sequence 47, Application US/08410779B
; Patent No. 5814517
;  GENERAL INFORMATION:
;    APPLICANT:  SEIDEL, H. MARTI
;    APPLICANT:  LAMB, I. PETER
;    TITLE OF INVENTION:  DNA SPACER REGULATORY ELEMENTS
;    TITLE OF INVENTION:  RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  166
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LIGAND PHARMACEUTICALS INCORPORATED
;      STREET:  9393 TOWNE CENTRE DRIVE
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  US
;      ZIP:  92121
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/410,779B
;      FILING DATE:  27-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/228,935
;      FILING DATE:  14-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JURGENSEN, THOMAS E
;      REGISTRATION NUMBER:  34,195
;      REFERENCE/DOCKET NUMBER:  016-0013A.US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 550-7675
;      TELEFAX:  (619) 535-3906
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
US-08-410-779B-47

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 6.8;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              | ||||||||
Db          1 TTCCCAAGAA 10


RESULT 5
US-09-508-753B-225/c
; Sequence 225, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 225
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-225

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 6.8;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCAAGA 1030
              |||| |||||
Db         10 CTGCTCAAGA 1


RESULT 6
PCT-US95-04477-47
; Sequence 47, Application PC/TUS9504477
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO
;    TITLE OF INVENTION:  CYTOKINES AND METHODS FOR THEIR USE
;    NUMBER OF SEQUENCES:  165
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04477
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/228,935
;      FILING DATE:  14-APR-1994
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OTHER NUCLEIC ACID,
;      DESCRIPTION:  SYNTHETIC DNA"
PCT-US95-04477-47

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 6.8;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              | ||||||||
Db          1 TTCCCAAGAA 10


RESULT 7
US-08-401-512-15
; Sequence 15, Application US/08401512
; Patent No. 5599673
;  GENERAL INFORMATION:
;    APPLICANT:  Keating, Mark T.
;    APPLICANT:  Curran, Mark E.
;    APPLICANT:  Wang, Qing
;    TITLE OF INVENTION:  Long QT Syndrome Genes
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Venable, Baetjer, Howard & Civiletti,LLP
;      STREET:  1201 New York Avenue, Suite 1000
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3917
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,512
;      FILING DATE:  09-MAR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Saxe, Stephen A.
;      REGISTRATION NUMBER:  38,609
;      REFERENCE/DOCKET NUMBER:  19780-113879
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-962-4848
;      TELEFAX:  202-962-8300
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-401-512-15

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGGAGGTGGG 10


RESULT 8
US-08-481-658B-73
; Sequence 73, Application US/08481658B
; Patent No. 5955075
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  6 Mariposa Court
;      CITY:  Tiburon
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94920
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/481,658B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-481-658B-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 9
US-08-477-504A-73
; Sequence 73, Application US/08477504A
; Patent No. 5972353
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  6 Mariposa Court
;      CITY:  Tiburon
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94920
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/477,504A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-477-504A-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 10
US-08-486-756A-73
; Sequence 73, Application US/08486756A
; Patent No. 5981711
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  6 Mariposa Court
;      CITY:  Tiburon
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94920
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/486,756A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-486-756A-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 11
US-08-485-862B-73
; Sequence 73, Application US/08485862B
; Patent No. 5989838
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  6 Mariposa Court
;      CITY:  Tiburon
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94920
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,862B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,504
;      FILING DATE:  07-JUN-1995
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3D
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-485-862B-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 12
US-08-787-739-73
```

```
; Sequence 73, Application US/08787739
; Patent No. 6027887
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  96
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  369 Pine Street, Suite 610
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/787,739
;      FILING DATE:  24-JAN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/485,049
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/486,756
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/477,504
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/481,658
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/485,862
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/485,863
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/487,077
;      FILING DATE:  07-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-981-2034
;      TELEFAX:  415-981-0332
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-787-739-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 13
US-08-487-077A-73
; Sequence 73, Application US/08487077A
; Patent No. 6069242
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  6 Mariposa Court
;      CITY:  Tiburon
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94920
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,077A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3H
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-487-077A-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 14
US-08-485-863A-73
; Sequence 73, Application US/08485863A
; Patent No. 6093548
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  6 Mariposa Court
;      CITY:  Tiburon
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94920
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,863A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-435-2034
;      TELEFAX:  415-435-0727
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-485-863A-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 15
US-08-485-049D-73
; Sequence 73, Application US/08485049D
; Patent No. 6204370
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  369 Pine Street
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,049D
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/260,190
;      FILING DATE:  15-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lauder, Leona L.
;      REGISTRATION NUMBER:  30,863
;      REFERENCE/DOCKET NUMBER:  D-0021.3E
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-981-2034
;      TELEFAX:  415-981-0332
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;      DESCRIPTION:  5' donor consensus splice sequence
US-08-485-049D-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 16
US-09-178-115-73
; Sequence 73, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT: Pastorekova, Silvia
;  APPLICANT: Pastorek, Jaromir
;  TITLE OF INVENTION: MN Gene and Protein
;  FILE REFERENCE: D-0021.5A
;  CURRENT APPLICATION NUMBER: US/09/178,115
;  CURRENT FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 09/177,776
;  EARLIER FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 08/787,739
;  EARLIER FILING DATE: 1997-01-24
;  EARLIER APPLICATION NUMBER: 08/485,049
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/486,756
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/477,504
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/481,658
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/485,862
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/485,863
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/487,077
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/260,190
;  EARLIER FILING DATE: 1994-06-15
;  EARLIER APPLICATION NUMBER: 08/177,093
;  EARLIER FILING DATE: 1993-12-30
;  EARLIER APPLICATION NUMBER: 07/964,589
;  EARLIER FILING DATE: 1992-10-21
;  EARLIER APPLICATION NUMBER: PV-709-92
;  EARLIER FILING DATE: 1992-03-11
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-178-115-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 17
US-09-177-776-73
```

```
; Sequence 73, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT: Pastorekova, Silvia
;  APPLICANT: Pastorek, Jaromir
;  TITLE OF INVENTION: MN Gene and Protein
;  FILE REFERENCE: D-0021.5A
;  CURRENT APPLICATION NUMBER: US/09/177,776A
;  CURRENT FILING DATE: 1998-10-23
;  EARLIER APPLICATION NUMBER: 08/787,739
;  EARLIER FILING DATE: 1997-01-24
;  EARLIER APPLICATION NUMBER: 08/485,049
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/486,756
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/477,504
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/481,658
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/485,862
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/485,863
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/487,077
;  EARLIER FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 08/260,190
;  EARLIER FILING DATE: 1994-06-15
;  EARLIER APPLICATION NUMBER: 08/177,093
;  EARLIER FILING DATE: 1993-12-30
;  EARLIER APPLICATION NUMBER: 07/964,589
;  EARLIER FILING DATE: 1992-10-21
;  EARLIER APPLICATION NUMBER: PV-709-92
;  EARLIER FILING DATE: 1992-03-11
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-177-776-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 18
US-09-772-719B-73
; Sequence 73, Application US/09772719B
; Patent No. 6770438
;   GENERAL INFORMATION:
;        APPLICANT: Zavada, Jan
;                   Pastorekova, Silvia
;                   Pastorek, Jaromir
;        TITLE OF INVENTION: MN Gene and Protein
;        NUMBER OF SEQUENCES: 86
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Leona L. Lauder
;             STREET: 465 California Street, Suite 450
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/772,719B
;             FILING DATE: 30-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/485,049
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Lauder, Leona L.
;             REGISTRATION NUMBER: 30,863
;             REFERENCE/DOCKET NUMBER: D-0021.3A-2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-981-2034
;             TELEFAX: 415-981-0332
;   INFORMATION FOR SEQ ID NO: 73:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 11 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;             DESCRIPTION: 5' donor consensus splice sequence
;        SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-772-719B-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 6.2;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 19
US-08-049-283A-31
; Sequence 31, Application US/08049283A
; Patent No. 5502176
;  GENERAL INFORMATION:
;    APPLICANT:  Tenen, Daniel G.
;    APPLICANT:  Pahl, Heike L.
;    APPLICANT:  Burn, Timothy C.
;    TITLE OF INVENTION:  Cell Specific Promoter and Uses Thereof
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.c.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/049,283A
;      FILING DATE:  14-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/020,465
;      FILING DATE:  19-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/837,776
;      FILING DATE:  13-FEB-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  BIH91-03'A
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-049-283A-31

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
             ||||||||
Db          1 CTTCTGCC 8


RESULT 20
US-08-049-283A-33
; Sequence 33, Application US/08049283A
; Patent No. 5502176
;  GENERAL INFORMATION:
;    APPLICANT:  Tenen, Daniel G.
;    APPLICANT:  Pahl, Heike L.
;    APPLICANT:  Burn, Timothy C.
;    TITLE OF INVENTION:  Cell Specific Promoter and Uses Thereof
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.c.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/049,283A
;      FILING DATE:  14-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/020,465
;      FILING DATE:  19-FEB-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/837,776
;      FILING DATE:  13-FEB-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  BIH91-03'A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-049-283A-33

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
             ||||||||
Db          3 TTCTGCCC 10


RESULT 21
US-09-508-753B-70
; Sequence 70, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
;  APPLICANT: Akira SHIMAMOTO
;  APPLICANT:  Yasuhiro FURUICHI
;  APPLICANT:  Yuko SHIBATA
;  APPLICANT:  Hiroko FUNAKI
;  APPLICANT:  Eiji OHARA
;  APPLICANT:  Masanori WATAHIKI
;  TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
;  FILE REFERENCE: 00162/HG
;  CURRENT APPLICATION NUMBER: US/09/508,753B
;  CURRENT FILING DATE:  2000-06-16
;  PRIOR APPLICATION NUMBER: JP 9/270324
;  PRIOR FILING DATE: 1997-09-18
;  NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 70
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-70

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
             ||||||||
Db          3 TTCTGCCC 10


RESULT 22
US-08-437-013-6
; Sequence 6, Application US/08437013
; Patent No. 5932220
;  GENERAL INFORMATION:
;    APPLICANT:  Barbour, Alan G.
;    APPLICANT:  Carter, Carol
;    TITLE OF INVENTION:  Diagnostic Tests for a New Spriochete, Borrelia
;    TITLE OF INVENTION:  lonestari sp. nov.
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  US
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/437,013
;      FILING DATE:  08-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mayfield, Denise L.
;      REGISTRATION NUMBER:  33,732
;      REFERENCE/DOCKET NUMBER:  UTSK:276/MAY
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-300
```

```
;      TELEFAX:  512/747-7577
;      TELEX:  NA
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "DNA"
US-08-437-013-6

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 50;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAA 1028
              ||||| |||
Db          1 TCTGCTCAA 9


RESULT 23
US-09-275-506A-6
; Sequence 6, Application US/09275506A
; Patent No. 6617441
; GENERAL INFORMATION:
;  APPLICANT: BARBOUR, ALAN G.
;  APPLICANT:  CARTER, CAROL
;  TITLE OF INVENTION: A DIAGNOSTIC TEST FOR INFECTION WITH A SPIROCHETE BORNE
;  TITLE OF INVENTION:  BY AMBLYOMMA AMERICANIUM
;  FILE REFERENCE: UTSK:352
;  CURRENT APPLICATION NUMBER: US/09/275,506A
;  CURRENT FILING DATE:  1999-03-24
;  PRIOR APPLICATION NUMBER: 08/437,013
;  PRIOR FILING DATE: 1995-05-08
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Primer
US-09-275-506A-6

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 50;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAA 1028
              ||||| |||
Db          1 TCTGCTCAA 9


RESULT 24
US-09-639-576-2
; Sequence 2, Application US/09639576
; Patent No. 6720167
; GENERAL INFORMATION:
;  APPLICANT: Federici, Brian A.
;  APPLICANT:  Bideshi, Dennis K.
;  APPLICANT:  Park, Hyun-Woo
;  APPLICANT:  Wirth, Margaret C.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Improved Insecticidal Bacteria, and Methods for Making
;  TITLE OF INVENTION:  and Using Them
;  FILE REFERENCE: 023070-113500US
;  CURRENT APPLICATION NUMBER: US/09/639,576
;  CURRENT FILING DATE:  2000-08-14
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:STAB-SD from
;   OTHER INFORMATION: Bacillus thuringiensis cry3B gene
US-09-639-576-2

  Query Match             37.0%;  Score 7.4;  DB 1;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 50;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              ||||| |||
Db          1 GAAGGGGGG 9


RESULT 25
US-08-593-345B-19
; Sequence 19, Application US/08593345B
; Patent No. 5851772
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Lysov, Yuriy P
;    APPLICANT:  Shick, Valentine V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  A Microchip Method for the Enrichment of
;    TITLE OF INVENTION:  Specific DNA Sequences.
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh 7.1
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/593,345B
;      FILING DATE:  29-JAN-96
;    PRIOR APPLICATION DATA:  No. 5851772e
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-029+30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 5851772 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    FEATURE:
;      NAME/KEY:  No. 5851772e
;      LOCATION:  1-8
;      IDENTIFICATION METHOD:  Similarity with known sequences.
;      OTHER INFORMATION:  Complementarity with primer of
;      OTHER INFORMATION:  exons to a-thalassemia gene.
US-08-593-345B-19

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGA 1030
              |||||||
```

```
Db          1 CCCAAGA 7


RESULT 26
US-08-859-954-55
; Sequence 55, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-55

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAA 1028
             |||||||
Db          2 TGCCCAA 8


RESULT 27
US-08-859-954-248
; Sequence 248, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  248:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-248

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTG 1035
             |||||||
Db          1 GAAGGTG 7


RESULT 28
US-08-859-954-249
; Sequence 249, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  249:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-249

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTG 1035
             |||||||
Db          1 GAAGGTG 7


RESULT 29
US-08-859-954-267
; Sequence 267, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  267:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-267

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGG 1033
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Db          2 AAGAAGG 8


RESULT 30
US-08-859-954-406
; Sequence 406, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  406:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-406

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAA 1028
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Db          2 TGCCCAA 8
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RESULT 31
US-08-859-954-540
; Sequence 540, Application US/08859954
; Patent No. 6083695
;  GENERAL INFORMATION:
;    APPLICANT:  Hardin, Susan H.
;    APPLICANT:  Homayouni, Ramin
;    APPLICANT:  Hardin, Paul E.
;    TITLE OF INVENTION:  Design and Optimized Primer Library for
;    TITLE OF INVENTION:  Gene Sequencing and Method Thereof
;    NUMBER OF SEQUENCES:  566
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski L.L.P.
;      STREET:  1301 McKinney, Suite 5100
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  U.S.A.
;      ZIP:  77010-3095
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,954
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/632,782
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul, Thomas D.
;      REGISTRATION NUMBER:  32,714
;      REFERENCE/DOCKET NUMBER:  D-5900
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  713/651-5325
;      TELEFAX:  713/651-5246
;  INFORMATION FOR SEQ ID NO:  540:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "oligonucleotide"
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
US-08-859-954-540

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGG 1036
             |||||||
Db          1 AAGGTGG 7


RESULT 32
US-08-855-372B-6
; Sequence 6, Application US/08855372B
; Patent No. 6090549
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous Stacking Hybridization as a Diagn
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/855,372B
;      FILING DATE:  13-MAY-97
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6090549 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-08-855-372B-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCA 1027
             |||||||
Db          1 CTGCCCA 7


RESULT 33
US-09-498-851-6
; Sequence 6, Application US/09498851
; Patent No. 6440671
;  GENERAL INFORMATION:
;    APPLICANT:  Mirzabekov, Andrei D
;    APPLICANT:  Parinov, Sergei V
;    APPLICANT:  Barsky, Victor E
;    APPLICANT:  Kirillov, Eugene V
;    APPLICANT:  Dubiley, Svetlana A
;    TITLE OF INVENTION:  Use of Continuous/Contiguous
;    TITLE OF INVENTION:  Stacking Hybridization as a Diagnostic Tool.
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHERSKOV & FLAYNIK
;      STREET:  20 N. Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.50 inch, 1.4 MB storage
;      COMPUTER:  PC
;      OPERATING SYSTEM:  Microsoft Windows 98
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/498,851
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/855,372
;      FILING DATE:  13-MAY-97
```

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;      APPLICATION NUMBER:  U.S. 08/587,332
;      FILING DATE:  16-JAN-96
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cherskov, Michael J.
;      REGISTRATION NUMBER:  33,664
;      REFERENCE/DOCKET NUMBER:  ANL-IN-95-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 621-1330
;      TELEFAX:  (312) 621-0088
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  No. 6440671 Applicable
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  yes
US-09-498-851-6

  Query Match             35.0%;  Score 7;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 57;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1021 CTGCCCA 1027
             |||||||
Db          1 CTGCCCA 7


RESULT 34
US-08-068-945A-36/c
; Sequence 36, Application US/08068945A
; Patent No. 5616483
;  GENERAL INFORMATION:
;    APPLICANT:  Bjursell, Gunnar
;    APPLICANT:  Carlsson, Peter
;    APPLICANT:  Enerback, Sven
;    APPLICANT:  Hansson, Lennart
;    APPLICANT:  Lidberg, Ulf
;    APPLICANT:  Nilsson, Jeanette
;    APPLICANT:  Tornell, Jan
;    TITLE OF INVENTION:  New DNA Sequences
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White & Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/068,945A
;      FILING DATE:  27-MAY-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9201809-2
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9201826-6
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9202088-2
;      FILING DATE:  03-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9300902-5
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J.
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-052
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8783
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-068-945A-36

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAA 1031
             |||||||
Db          8 CCAAGAA 2


RESULT 35
US-08-442-806-36/c
; Sequence 36, Application US/08442806
; Patent No. 5716817
;  GENERAL INFORMATION:
;    APPLICANT:  Bjursell, Gunnar
;    APPLICANT:  Carlsson, Peter
;    APPLICANT:  Enerback, Sven
;    APPLICANT:  Hansson, Lennart
;    APPLICANT:  Lidberg, Ulf
;    APPLICANT:  Nilsson, Jeanette
;    APPLICANT:  Tornell, Jan
;    TITLE OF INVENTION:  Genomic DNA Sequences
;    TITLE OF INVENTION:  Encoding Human BSSL/CEL
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  White & Case
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  10036-2787
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/442,806
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/068,945
;      FILING DATE:  27-MAY-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9201809-2
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9201826-6
;      FILING DATE:  12-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9202088-2
;      FILING DATE:  03-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  SE 9300902-5
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sterner, Richard J.
;      REGISTRATION NUMBER:  35,372
;      REFERENCE/DOCKET NUMBER:  1103326-052
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)819-8783
;      TELEFAX:  (212)354-8113
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-442-806-36

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAA 1031
             |||||||
Db          8 CCAAGAA 2


RESULT 36
US-09-063-450-10
; Sequence 10, Application US/09063450
; Patent No. 6109776
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: Method and System for Computationally Identifying
;  TITLE OF INVENTION: Clusters Within a Set of Sequences
;  FILE REFERENCE: 77001.002
;  CURRENT APPLICATION NUMBER: US/09/063,450
;  CURRENT FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:example
;   OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-10

  Query Match             35.0%;  Score 7;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTG 1035
             |||||||
Db          3 GAAGGTG 9


Search completed: December  3, 2004, 11:41:57
Job time : 1 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:43:49 ; Search time 0.001 Seconds
(without alignments)
21.120 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cttctgcccaagaaggtggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 50 seqs, 528 residues

Total number of hits satisfying chosen parameters: 100

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : rnpbdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	20	1	US-10-024-369-47	Sequence 47, Appl
	2	12.8	64.0	17	1	US-09-930-423-674	Sequence 674, App
	3	12.8	64.0	17	1	US-09-745-237A-674	Sequence 674, App
c	4	12	60.0	15	1	US-09-775-818-2	Sequence 2, Appli
c	5	12	60.0	15	1	US-10-663-999-2	Sequence 2, Appli
	6	9.4	47.0	12	1	US-10-661-165-445	Sequence 445, App
	7	9	45.0	10	1	US-10-033-145-410	Sequence 410, App
	8	9	45.0	10	1	US-10-033-145-930	Sequence 930, App
	9	9	45.0	10	1	US-10-033-145-1231	Sequence 1231, Ap
c	10	9	45.0	11	1	US-09-862-847-15	Sequence 15, Appl
c	11	8.4	42.0	10	1	US-10-033-145-262	Sequence 262, App
c	12	8.4	42.0	10	1	US-10-033-145-437	Sequence 437, App
	13	8.4	42.0	10	1	US-10-033-145-2081	Sequence 2081, Ap
c	14	8.4	42.0	10	1	US-10-057-726-3	Sequence 3, Appli
	15	8.4	42.0	10	1	US-10-330-627-713	Sequence 713, App
	16	8.4	42.0	10	1	US-10-293-222-330	Sequence 330, App
c	17	8.4	42.0	10	1	US-10-660-253-84	Sequence 84, Appl
c	18	8.4	42.0	10	1	US-10-670-011-398	Sequence 398, App
	19	8.4	42.0	11	1	US-09-772-719-73	Sequence 73, Appl
	20	8.4	42.0	11	1	US-09-967-237-73	Sequence 73, Appl
	21	8.4	42.0	11	1	US-10-450-797-170	Sequence 170, App
c	22	8.4	42.0	11	1	US-10-450-797-1255	Sequence 1255, Ap
c	23	8.4	42.0	11	1	US-10-450-797-1259	Sequence 1259, Ap
	24	8	40.0	9	1	US-09-989-789-2078	Sequence 2078, Ap
	25	8	40.0	9	1	US-09-989-789-2079	Sequence 2079, Ap
	26	8	40.0	9	1	US-09-989-789-2262	Sequence 2262, Ap
	27	8	40.0	9	1	US-09-989-789-2263	Sequence 2263, Ap
c	28	8	40.0	9	1	US-09-846-033B-7	Sequence 7, Appli
	29	8	40.0	9	1	US-09-990-186-2078	Sequence 2078, Ap
	30	8	40.0	9	1	US-09-990-186-2079	Sequence 2079, Ap
	31	8	40.0	9	1	US-09-990-186-2262	Sequence 2262, Ap
	32	8	40.0	9	1	US-09-990-186-2263	Sequence 2263, Ap
	33	8	40.0	9	1	US-09-989-994-2078	Sequence 2078, Ap
	34	8	40.0	9	1	US-09-989-994-2079	Sequence 2079, Ap
	35	8	40.0	9	1	US-09-989-994-2262	Sequence 2262, Ap
	36	8	40.0	9	1	US-09-989-994-2263	Sequence 2263, Ap
c	37	8	40.0	9	1	US-10-006-069A-7	Sequence 7, Appli
c	38	8	40.0	10	1	US-10-033-145-198	Sequence 198, App
c	39	8	40.0	10	1	US-10-033-145-296	Sequence 296, App
c	40	8	40.0	10	1	US-10-033-145-298	Sequence 298, App
	41	8	40.0	10	1	US-10-033-145-701	Sequence 701, App
c	42	8	40.0	10	1	US-10-033-145-1370	Sequence 1370, Ap
c	43	8	40.0	10	1	US-10-033-145-1792	Sequence 1792, Ap
	44	8	40.0	10	1	US-10-033-145-1806	Sequence 1806, Ap
	45	8	40.0	10	1	US-10-033-145-1979	Sequence 1979, Ap
	46	8	40.0	10	1	US-10-010-802-281	Sequence 281, App
c	47	8	40.0	10	1	US-10-330-627-132	Sequence 132, App
	48	8	40.0	10	1	US-10-330-627-1157	Sequence 1157, Ap
	49	8	40.0	10	1	US-10-293-222-324	Sequence 324, App
c	50	8	40.0	10	1	US-10-215-982-360	Sequence 360, App

ALIGNMENTS

RESULT 1
US-10-024-369-47/c
; Sequence 47, Application US/10024369
; Publication No. US20030134809A1
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Donna T. Ward
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION
; FILE REFERENCE: RTS-0353
; CURRENT APPLICATION NUMBER: US/10/024,369
; CURRENT FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-369-47

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1018 CTTCTGCCCAAGAAGGTGGG 1037
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Db         20 CTTCTGCCCAAGAAGGTGGG 1
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RESULT 2
US-09-930-423-674
; Sequence 674, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 674
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-674

Query Match 64.0%; Score 12.8; DB 1; Length 17;

```
  Best Local Similarity   68.8%;  Pred. No. 2.9;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAAGAAGGTG 1035
              : :||||||||| |:|
Db          2 UUUGCCCAAGAAAGUG 17


RESULT 3
US-09-745-237A-674
; Sequence 674, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
;  FILE REFERENCE: 400/007 (MBHB00-918-A)
;  CURRENT APPLICATION NUMBER: US/09/745,237A
;  CURRENT FILING DATE:  2002-04-15
;  NUMBER OF SEQ ID NOS: 4550
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 674
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-745-237A-674

  Query Match             64.0%;  Score 12.8;  DB 1;  Length 17;
  Best Local Similarity   68.8%;  Pred. No. 2.9;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAAGAAGGTG 1035
              : :||||||||| |:|
Db          2 UUUGCCCAAGAAAGUG 17


RESULT 4
US-09-775-818-2/c
; Sequence 2, Application US/09775818
; Patent No. US20010044100A1
; GENERAL INFORMATION:
;  APPLICANT: Laboratory of Molecular Biophotonics
;  TITLE OF INVENTION: Method for selectively separating live cells expressing
;  TITLE OF INVENTION:  a specific gene
;  FILE REFERENCE: FP00-0043-00
;  CURRENT APPLICATION NUMBER: US/09/775,818
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: JP 2000/028117
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: JP 2000/130793
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe
US-09-775-818-2

  Query Match             60.0%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAAGG 1033
              ||||||||||||
Db         14 TGCCCAAGAAGG 3


RESULT 5
US-10-663-999-2/c
; Sequence 2, Application US/10663999
; Publication No. US20040161771A1
; GENERAL INFORMATION:
;  APPLICANT: Laboratory of Molecular Biophotonics
;  TITLE OF INVENTION: Method for selectively separating live cells expressing
;  TITLE OF INVENTION:  a specific gene
;  FILE REFERENCE: FP00-0043-00
;  CURRENT APPLICATION NUMBER: US/10/663,999
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US/09/775,818
;  PRIOR FILING DATE: 2000-04-28
;  PRIOR APPLICATION NUMBER: JP 2000/028117
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: JP 2000/130793
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Probe
US-10-663-999-2

  Query Match             60.0%;  Score 12;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAAGG 1033
              ||||||||||||
Db         14 TGCCCAAGAAGG 3


RESULT 6
US-10-661-165-445
; Sequence 445, Application US/10661165
; Publication No. US20040137470A1
; GENERAL INFORMATION:
;  APPLICANT: Dhallan, Ravinder S.
;  TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
;  TITLE OF INVENTION:  DISORDERS
;  FILE REFERENCE: 543312000420
;  CURRENT APPLICATION NUMBER: US/10/661,165
;  CURRENT FILING DATE:  2003-09-11
;  PRIOR APPLICATION NUMBER: PCT/US03/06198
;  PRIOR FILING DATE: 2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/378,354
;  PRIOR FILING DATE: 2002-05-08
;  PRIOR APPLICATION NUMBER: US 10/093,618
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US 60/360,232
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: PCT/US03/27308
;  PRIOR FILING DATE: 2003-08-29
;  PRIOR APPLICATION NUMBER: US 10/376,770
;  PRIOR FILING DATE: 2003-02-28
;  NUMBER OF SEQ ID NOS: 628
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 445
;   LENGTH: 12
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Primer
US-10-661-165-445

  Query Match             47.0%;  Score 9.4;  DB 1;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 10;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCCCAA 1028
              || ||||||||
```

```
Db          2 CTACTGCCCAA 12


RESULT 7
US-10-033-145-410
; Sequence 410, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 410
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-410

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGGG 1037
              |||||||||
Db          1 GAAGGTGGG 9


RESULT 8
US-10-033-145-930
; Sequence 930, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 930
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-930

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCCA 1027
              |||||||||
Db          2 TTCTGCCCA 10


RESULT 9
US-10-033-145-1231
; Sequence 1231, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1231
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1231

  Query Match             45.0%;  Score 9;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGG 1036
              |||||||||
Db          2 AGAAGGTGG 10


RESULT 10
US-09-862-847-15/c
; Sequence 15, Application US/09862847
; Patent No. US20020177230A1
; GENERAL INFORMATION:
;  APPLICANT: Baric, Ralph S.
;  APPLICANT:  Boyd, Yount
;  TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
;  FILE REFERENCE: 5470.270
;  CURRENT APPLICATION NUMBER: US/09/862,847
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: US 60/206,537
;  PRIOR FILING DATE: 2000-05-21
;  PRIOR APPLICATION NUMBER: US 60/285,320
;  PRIOR FILING DATE: 2001-04-20
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

  Query Match             45.0%;  Score 9;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1025 CCAAGAAGG 1033
              |||||||||
Db         10 CCAAGAAGG 2


RESULT 11
US-10-033-145-262/c
; Sequence 262, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
```

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; SEQ ID NO 262
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-262

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1022 TGCCCAAGAA 1031
              ||||||||  |
Db         10 TGCCCAAGCA 1


RESULT 12
US-10-033-145-437/c
; Sequence 437, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 437
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-437

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||| ||||||
Db         10 AAGCAGGTGG 1


RESULT 13
US-10-033-145-2081
; Sequence 2081, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2081
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-2081

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              ||| ||||||
Db          1 AGAGGGTGGG 10


RESULT 14
US-10-057-726-3/c
; Sequence 3, Application US/10057726
; Publication No. US20030017549A1
; GENERAL INFORMATION:
;  APPLICANT: Owens, Gary K.
;  APPLICANT:  Manabe, Ichiro
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSING POLYNUCLEOTIDES
;  TITLE OF INVENTION:  SPECIFICALLY IN SMOOTH MUSCLE CELLS IN VIVO
;  FILE REFERENCE: 021258-000200US
;  CURRENT APPLICATION NUMBER: US/10/057,726
;  CURRENT FILING DATE:  2002-06-24
;  PRIOR APPLICATION NUMBER: US 60/263,811
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: US 09/600,319
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: WO PCT/US99/01038
;  PRIOR FILING DATE: 1999-01-15
;  PRIOR APPLICATION NUMBER: US 60/071,300
;  PRIOR FILING DATE: 1998-01-16
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CArG2 sequence
;   OTHER INFORMATION: to be mutated
US-10-057-726-3

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGAAGG 1033
              ||||| ||||
Db         10 CCCAAAAAGG 1


RESULT 15
US-10-330-627-713
; Sequence 713, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 713
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-713

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10
```

```
RESULT 16
US-10-293-222-330
; Sequence 330, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
;  APPLICANT: Versteeg, Rogier
;  APPLICANT:  Caron, Hubertus N.
;  TITLE OF INVENTION: MYC targets
;  FILE REFERENCE: 2183-5580US
;  CURRENT APPLICATION NUMBER: US/10/293,222
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: PCT/NL01/00361
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: EP 00201698.8
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: EP 00202284.6
;  PRIOR FILING DATE: 2000-06-29
;  NUMBER OF SEQ ID NOS: 455
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 330
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-293-222-330

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1023 GCCCAAGAAG 1032
              || |||||||
Db          1 GCACAAGAAG 10


RESULT 17
US-10-660-253-84/c
; Sequence 84, Application US/10660253
; Publication No. US20040115705A1
; GENERAL INFORMATION:
;  APPLICANT: Behlke, Mark A.
;  APPLICANT:  Lingyan, Huang
;  APPLICANT:  Owczarzy, Richard
;  APPLICANT:  Walder, Joseph A.
;  TITLE OF INVENTION: METHODS AND SYSTEMS FOR ESTIMATING THE MELTING TEMPERATURE (Tm) F
;  TITLE OF INVENTION:  POLYNUCLEOTIDE MOLECULES
;  FILE REFERENCE: 03988/100K297-US1
;  CURRENT APPLICATION NUMBER: US/10/660,253
;  CURRENT FILING DATE:  2003-09-11
;  PRIOR APPLICATION NUMBER: US 60/410,663
;  PRIOR FILING DATE: 2002-09-12
;  NUMBER OF SEQ ID NOS: 92
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-660-253-84

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              |||||| |||
Db         10 AAGAAGTTGG 1


RESULT 18
US-10-670-011-398/c
; Sequence 398, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Beigelman, Leonid
;  APPLICANT:  Pavco, Pamela
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
;  TITLE OF INVENTION:  Growth Factor and Vascular Endothelial Growth Factor Receptor
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/132 (MBHB02-742-G)
;  CURRENT APPLICATION NUMBER: US/10/670,011
;  CURRENT FILING DATE:  2003-09-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05022
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  PRIOR APPLICATION NUMBER: US60/363,124
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: US60/386,782
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US60/393,796
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US60/399,348
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: US60/406,784
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US60/408,378
;  PRIOR FILING DATE: 2002-09-05
;  PRIOR APPLICATION NUMBER: US60/409,293
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: US60/440,129
;  PRIOR FILING DATE: 2003-01-15
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 427
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 398
;   LENGTH: 10
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-670-011-398

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 14;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCAAG 1029
              ||| ||||||
Db         10 TCTCCCCAAG 1


RESULT 19
US-09-772-719-73
; Sequence 73, Application US/09772719
; Patent No. US20020137910A1
;  GENERAL INFORMATION:
;    APPLICANT:  Zavada, Jan
;    APPLICANT:  Pastorekova, Silvia
;    APPLICANT:  Pastorek, Jaromir
;    TITLE OF INVENTION:  MN Gene and Protein
;    NUMBER OF SEQUENCES:  86
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leona L. Lauder
;      STREET:  369 Pine Street
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/772,719
;       FILING DATE:  30-JAN-2001
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/485,049
;       FILING DATE:  07-JUN-1995
;       APPLICATION NUMBER:  US 08/260,190
;       FILING DATE:  15-JUN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lauder, Leona L.
;       REGISTRATION NUMBER:  30,863
;       REFERENCE/DOCKET NUMBER:  D-0021.3E
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-981-2034
;       TELEFAX:  415-981-0332
;   INFORMATION FOR SEQ ID NO:  73:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;       DESCRIPTION:  5' donor consensus splice sequence
US-09-772-719-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 20
US-09-967-237-73
; Sequence 73, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
;  APPLICANT: Zavada, Jan
;  APPLICANT:  Pastorekova, Silvia
;  APPLICANT:  Pastorek, Jaromir
;  TITLE OF INVENTION: MN Gene and Protein
;  FILE REFERENCE: D-0021.5B-2
;  CURRENT APPLICATION NUMBER: US/09/967,237
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 09/178,115
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: HUMAN
US-09-967-237-73

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTGGG 1037
              || |||||||
Db          1 AGCAGGTGGG 10


RESULT 21
US-10-450-797-170
; Sequence 170, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
;  APPLICANT: Petersohn, Dirk
;  APPLICANT:  Conradt, Marcus
;  APPLICANT:  Hofmann, Kay
;  TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
;  FILE REFERENCE: HENK-0041
;  CURRENT APPLICATION NUMBER: US/10/450,797
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: PCT/EP01/15178
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: DE 101 00 121.5
;  PRIOR FILING DATE: 2001-01-03
;  NUMBER OF SEQ ID NOS: 1435
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-450-797-170

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1027 AAGAAGGTGG 1036
              ||||| ||||
Db          2 AAGAAAGTGG 11


RESULT 22
US-10-450-797-1255/c
; Sequence 1255, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
;  APPLICANT: Petersohn, Dirk
;  APPLICANT:  Conradt, Marcus
;  APPLICANT:  Hofmann, Kay
;  TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
;  FILE REFERENCE: HENK-0041
;  CURRENT APPLICATION NUMBER: US/10/450,797
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: PCT/EP01/15178
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: DE 101 00 121.5
;  PRIOR FILING DATE: 2001-01-03
;  NUMBER OF SEQ ID NOS: 1435
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1255
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-450-797-1255

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              | ||||||||
Db         11 CCAGAAGGTG 2


RESULT 23
US-10-450-797-1259/c
; Sequence 1259, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
;  APPLICANT: Petersohn, Dirk
;  APPLICANT:  Conradt, Marcus
;  APPLICANT:  Hofmann, Kay
;  TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
;  FILE REFERENCE: HENK-0041
;  CURRENT APPLICATION NUMBER: US/10/450,797
;  CURRENT FILING DATE:  2003-12-04
```

```
;  PRIOR APPLICATION NUMBER: PCT/EP01/15178
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: DE 101 00 121.5
;  PRIOR FILING DATE: 2001-01-03
;  NUMBER OF SEQ ID NOS: 1435
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1259
;   LENGTH: 11
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-450-797-1259

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 11;
  Best Local Similarity   90.0%;  Pred. No. 15;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGGTG 1035
              ||| ||||||
Db         11 CAATAAGGTG 2


RESULT 24
US-09-989-789-2078
; Sequence 2078, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2078
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2078

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
              ||||||||
Db          1 AAGGTGGG 8


RESULT 25
US-09-989-789-2079
; Sequence 2079, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2079
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2079

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
              ||||||||
Db          1 AAGGTGGG 8


RESULT 26
US-09-989-789-2262
; Sequence 2262, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2262
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2262

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 27
US-09-989-789-2263
; Sequence 2263, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.20 / S11-US2
;  CURRENT APPLICATION NUMBER: US/09/989,789
;  CURRENT FILING DATE:  2002-03-25
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2263
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-989-789-2263

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 28
```

```
US-09-846-033B-7/c
; Sequence 7, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
;  APPLICANT: Rebar, Edward
;  APPLICANT:  Jamieson, Andrew
;  APPLICANT:  Liu, Qiang
;  APPLICANT:  Liu, Pei-Qi
;  APPLICANT:  Wolffe, Alan
;  APPLICANT:  Eisenberg, Stephen P.
;  APPLICANT:  Jarvis, Eric
;  APPLICANT:  Sangamo BioSciences, Inc.
;  TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
;  TITLE OF INVENTION:  Finger Proteins
;  FILE REFERENCE: 019496-005820US
;  CURRENT APPLICATION NUMBER: US/09/846,033B
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 09/733,604
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 09/736,083
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 252
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: target
US-09-846-033B-7

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCA 1027
              ||||||||
Db          8 TCTGCCCA 1


RESULT 29
US-09-990-186-2078
; Sequence 2078, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2078
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2078

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
              ||||||||
Db          1 AAGGTGGG 8


RESULT 30
US-09-990-186-2079
; Sequence 2079, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2079
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2079

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
              ||||||||
Db          1 AAGGTGGG 8


RESULT 31
US-09-990-186-2262
; Sequence 2262, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2262
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: example target
;   OTHER INFORMATION: DNA
US-09-990-186-2262

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
              ||||||||
Db          2 AGAAGGTG 9


RESULT 32
US-09-990-186-2263
; Sequence 2263, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
;  APPLICANT: LIU, Qiang
;  TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
;  TITLE OF INVENTION:  TRIPLETS BY ZINC FINGERS
;  FILE REFERENCE: 8325-0011.21 / S11-US3
;  CURRENT APPLICATION NUMBER: US/09/990,186
;  CURRENT FILING DATE:  2001-11-20
;  NUMBER OF SEQ ID NOS: 4085
;  SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 2263
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2263

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTG 1035
||||||||
Db 2 AGAAGGTG 9

RESULT 33
US-09-989-994-2078
; Sequence 2078, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2078
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2078

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1030 AAGGTGGG 1037
||||||||
Db 1 AAGGTGGG 8

RESULT 34
US-09-989-994-2079
; Sequence 2079, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2079
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2079

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1030 AAGGTGGG 1037
||||||||
Db 1 AAGGTGGG 8

RESULT 35
US-09-989-994-2262
; Sequence 2262, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2262
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2262

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTG 1035
||||||||
Db 2 AGAAGGTG 9

RESULT 36
US-09-989-994-2263
; Sequence 2263, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2263
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2263

Query Match 40.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1028 AGAAGGTG 1035
||||||||
Db 2 AGAAGGTG 9

RESULT 37
US-10-006-069A-7/c
; Sequence 7, Application US/10006069A
; Publication No. US20030021776A1

```
; GENERAL INFORMATION:
;  APPLICANT: Rebar, Edward
;  APPLICANT:  Jamieson, Andrew
;  APPLICANT:  Liu, Qiang
;  APPLICANT:  Liu, Pei-Qi
;  APPLICANT:  Wolffe, Alan
;  APPLICANT:  Eisenberg, Stephen P.
;  APPLICANT:  Jarvis, Eric
;  APPLICANT:  Sangamo BioSciences, Inc.
;  TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
;  TITLE OF INVENTION:  Finger Proteins
;  FILE REFERENCE: 019496-005830US
;  CURRENT APPLICATION NUMBER: US/10/006,069A
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: US 09/733,604
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 09/736,083
;  PRIOR FILING DATE: 2000-12-12
;  PRIOR APPLICATION NUMBER: US 09/846,033
;  PRIOR FILING DATE: 2001-04-30
;  NUMBER OF SEQ ID NOS: 252
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: target
US-10-006-069A-7

  Query Match             40.0%;  Score 8;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 89;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1020 TCTGCCCA 1027
             ||||||||
Db          8 TCTGCCCA 1


RESULT 38
US-10-033-145-198/c
; Sequence 198, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-198

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1019 TTCTGCCC 1026
             ||||||||
Db          8 TTCTGCCC 1


RESULT 39
US-10-033-145-296/c
; Sequence 296, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 296
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-296

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          9 AGAAGGTG 2


RESULT 40
US-10-033-145-298/c
; Sequence 298, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 298
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-298

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1030 AAGGTGGG 1037
             ||||||||
Db         10 AAGGTGGG 3


RESULT 41
US-10-033-145-701
; Sequence 701, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
```

```
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 701
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-701

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db             2 CTTCTGCC 9


RESULT 42
US-10-033-145-1370/c
; Sequence 1370, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1370
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1370

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db             8 CTTCTGCC 1


RESULT 43
US-10-033-145-1792/c
; Sequence 1792, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1792
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1792

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
              ||||||||
Db             8 CAAGAAGG 1


RESULT 44
US-10-033-145-1806
; Sequence 1806, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1806
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1806

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
              ||||||||
Db             2 CTTCTGCC 9


RESULT 45
US-10-033-145-1979
; Sequence 1979, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
;  APPLICANT: GENZYME CORPORATION
;  APPLICANT:  ROBERTS, BRUCE
;  APPLICANT:  SHANKARA, SRINIVAS
;  TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
;  FILE REFERENCE: GA0201C
;  CURRENT APPLICATION NUMBER: US/10/033,145
;  CURRENT FILING DATE:  2001-11-05
;  PRIOR APPLICATION NUMBER: PCT/US99/13800
;  PRIOR FILING DATE: 1999-06-18
;  NUMBER OF SEQ ID NOS: 2137
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1979
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-1979

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
              ||||||||
Db             2 GAAGGTGG 9


RESULT 46
US-10-010-802-281
; Sequence 281, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Genaissance Pharmaceuticals
;  APPLICANT:  Chew, Anne
;  APPLICANT:  Denton, R. Rex
;  APPLICANT:  Duda, Amy
;  APPLICANT:  Nandabalan, Krishnan
;  APPLICANT:  Stephens, J. Claiborne
;  APPLICANT:  Windemuth, Andreas
;  TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin
;  TITLE OF INVENTION:  4 Receptor Alpha Gene
;  FILE REFERENCE: MWH-0002US2 IL4R alpha
;  CURRENT APPLICATION NUMBER: US/10/010,802
;  CURRENT FILING DATE:  2001-11-09
;  PRIOR APPLICATION NUMBER: PCT/US00/19094
;  PRIOR FILING DATE: 2000-07-13
;  NUMBER OF SEQ ID NOS: 413
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 281
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-010-802-281

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 GAAGGTGG 1036
             ||||||||
Db          3 GAAGGTGG 10


RESULT 47
US-10-330-627-132/c
; Sequence 132, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 132
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-132

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1026 CAAGAAGG 1033
             ||||||||
Db          8 CAAGAAGG 1


RESULT 48
US-10-330-627-1157
; Sequence 1157, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
;  APPLICANT: Velculescu, Victor E.
;  APPLICANT:  Kinzler, Kenneth W
;  APPLICANT:  Vogelstein, Bert
;  TITLE OF INVENTION: Human Transcriptomes
;  FILE REFERENCE: 001107.00319
;  CURRENT APPLICATION NUMBER: US/10/330,627
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 09/448,480
;  PRIOR FILING DATE: 1999-11-24
;  NUMBER OF SEQ ID NOS: 1564
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1157
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-330-627-1157

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1028 AGAAGGTG 1035
             ||||||||
Db          3 AGAAGGTG 10


RESULT 49
US-10-293-222-324
; Sequence 324, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
;  APPLICANT: Versteeg, Rogier
;  APPLICANT:  Caron, Hubertus N.
;  TITLE OF INVENTION: MYC targets
;  FILE REFERENCE: 2183-5580US
;  CURRENT APPLICATION NUMBER: US/10/293,222
;  CURRENT FILING DATE:  2002-11-12
;  PRIOR APPLICATION NUMBER: PCT/NL01/00361
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: EP 00201698.8
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: EP 00202284.6
;  PRIOR FILING DATE: 2000-06-29
;  NUMBER OF SEQ ID NOS: 455
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 324
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-293-222-324

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1018 CTTCTGCC 1025
             ||||||||
Db          2 CTTCTGCC 9


RESULT 50
US-10-215-982-360/c
; Sequence 360, Application US/10215982
; Publication No. US20040219523A1
; GENERAL INFORMATION:
;  APPLICANT: Stanton, Martin
;  APPLICANT:  Epstein, David
;  APPLICANT:  Hamaguchi, Nobuko
;  APPLICANT:  Kurz, Markus
;  APPLICANT:  Keefe, Tony
;  APPLICANT:  Wilson, Charles
;  APPLICANT:  Grate, Dilara
;  APPLICANT:  Marshall, Kristin
;  APPLICANT:  McCauley, Thomas
;  APPLICANT:  Kurz, Jeffrey
;  TITLE OF INVENTION: NUCLEIC ACID SENSOR MOLECULES AND METHODS OF USING SAME
;  FILE REFERENCE: 23239-501 CIP
;  CURRENT APPLICATION NUMBER: US/10/215,982
;  CURRENT FILING DATE:  2002-08-09
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;  PRIOR APPLICATION NUMBER: 60/232,454
;  PRIOR FILING DATE: 2000-09-13
;  PRIOR APPLICATION NUMBER: 09/952,680
;  PRIOR FILING DATE: 2001-09-13
;  PRIOR APPLICATION NUMBER: 60/311,378
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: 60/313,932
;  PRIOR FILING DATE: 2001-08-21
;  PRIOR APPLICATION NUMBER: 60/338,186
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: 60/349,959
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: 60/364,486
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/376,744
;  PRIOR FILING DATE: 2002-05-01
;  PRIOR APPLICATION NUMBER: 60/367,991
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: 60/369,887
;  PRIOR FILING DATE: 2002-04-04
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 372
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 360
;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Exon 1, the
;   OTHER INFORMATION: 5'-exon
US-10-215-982-360

  Query Match             40.0%;  Score 8;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1024 CCCAAGAA 1031
              ||||||||
Db          9 CCCAAGAA 2


Search completed: December  3, 2004, 11:43:49
Job time : 0.001 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:48:01 ; Search time 0.001 Seconds
(without alignments)
0.640 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cttctgcccaagaaggtggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 16 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : rstdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	7	35.0	8	1	CL677992	ACCESSION:CL677992
2	6	30.0	8	1	CA851350	ACCESSION:CA851350

ALIGNMENTS

RESULT 1
CL677992/c
LOCUS CL677992 8 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0121d_B07_2 - PRI0121d.BR (8) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL677992
VERSION CL677992.1 GI:50184054
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 8)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .8
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 35.0%; Score 7; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1029 GAAGGTG 1035
              |||||||
Db          7 GAAGGTG 1
```

RESULT 2
CA851350
LOCUS CA851350 8 bp mRNA linear EST 01-AUG-2003
DEFINITION D12G08_N20_14.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D12G08 5', mRNA sequence.
ACCESSION CA851350
VERSION CA851350.1 GI:33388143
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 8)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
FEATURES Location/Qualifiers
source 1. .8
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D12G08"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

Query Match 30.0%; Score 6; DB 1; Length 8;
Best Local Similarity 85.7%; Pred. No. 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1024 CCCAAGA 1030
              ||||| |
Db          2 CCCAANA 8
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Search completed: December 3, 2004, 11:48:01
Job time : 0.001 secs